

CC fertility, flower development and morphology. FT or TFL1 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is rice MADS box-like
 CC protein. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 224 AA;

Query Match 58.2%; Score 684.5; DB 5; Length 224;
 Best Local Similarity 60.8%; Pred. No. 2.2e-57;
 Matches 138; Conservative 34; Mismatches 50; Indels 5; Gaps 5;

QY 1 MGRGKLEIKKINPNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 DB 1 MGRGKLEIKKINPNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 QY 61 STDIGKIERVYQVVTGMDLMAQYERMONTKHLNEINQNLKKEIRRRKGELEGMDIQ 120
 DB 61 STDIGKIERVYQVVTGMDLMAQYERMONTKHLNEINQNLKKEIRRRKGELEGMDIQ 120
 QY 121 LRGLQTLBESLRIVRRKHYVIAOTDTYKKKLSRTETRYALIHEDMKKEPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKHYVIAOTDTYKKKLSRTETRYALIHEDMKKEPNYGFN 180
 QY 181 VENQSRIVENSIPMVNCEPOMESFRVYHPNPNLGLGY-ESHDSL 226
 DB 179 VDNLTGGWGDGAG-AGAAADMFARVY-PSQPNLHGAYGNDLRL 223

RESULT 2
 AAB25755
 ID AAB25755 standard; protein; 227 AA.
 AC AAB25755;
 XX
 DT 04-NOV-2002 (first entry)
 XX
 DE Corn AP3 homologue protein from clone ctaln.pk0050.f8.
 XX
 KW Floral developmental protein; flowering locus T; APETALA3; transgenic;
 KW FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 KW tissue culture; cell division; corn.
 XX
 OS Zea mays.
 OS
 PN WO200244390-A2.
 XX
 PD 06-JUN-2002.
 XX
 PF 21-NOV-2001; 2001WO-US043750.
 XX
 FR 28-NOV-2000; 2000US-0253415P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Cahoon EB, Cahoon RE, Klein TM, Rafaleki AJ, Sakai H;
 XX
 DR WPI; 2002-547703/58.
 DR N-PSDB; AAD42257.
 XX
 PT New floral developmental polypeptide having flowering locus T or AP3
 PT homolog activity, useful for immunological screening of cDNA expression
 PT libraries.
 XX
 PS Claim 18; Page 78; 88pp; English.
 XX
 CC The present invention relates to novel floral developmental proteins,
 CC more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 CC proteins and polynucleotides encoding such proteins. (AP3) homologue
 CC polynucleotides are useful for transforming cells or for producing plants
 CC by transforming the plant cells with the polynucleotides and regenerating
 CC the plants from the transformed plant cells. Sequences of the invention

CC are useful for immunological screening of cDNA expression libraries. They
 CC are also useful for creating transgenic plants. Polynucleotides of the
 CC invention are used as probes for genetically and physically mapping the
 CC genes that they are a part of and as markers for traits linked to those
 CC genes. AP3 homologues may be useful for engineering plant sterility or
 CC fertility, flower development and morphology. FT or TFL1 homologues are
 CC useful for engineering flowering time, plant growth rate, inflorescence
 CC architecture, tissue culture morphology and rate of cell division to
 CC enhance transformation. The present sequence is corn AP3 homologue
 XX
 SQ Sequence 227 AA;

Query Match 57.3%; Score 675; DB 5; Length 227;
 Best Local Similarity 59.0%; Pred. No. 1.9e-56;
 Matches 135; Conservative 37; Mismatches 51; Indels 6; Gaps 5;

QY 1 MGRGKLEIKKINPNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 DB 1 MGRGKLEIKKINPNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
 QY 61 STDIGKIERVYQVVTGMDLMAQYERMONTKHLNEINQNLKKEIRRRKGELEGMDIQ 120
 DB 61 STDIGKIERVYQVVTGMDLMAQYERMONTKHLNEINQNLKKEIRRRKGELEGMDIQ 120
 QY 121 LRGLQTLBESLRIVRRKHYVIAOTDTYKKKLSRTETRYALIHEDMKKEPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKHYVIAOTDTYKKKLSRTETRYALIHEDMKKEPNYGFN 180
 QY 181 VENQSR-IVENSIPMVNCEPOMESFRVYHPNPNLGLGY-ESHDSL 226
 DB 179 VDNLTGGWGDGAG-AGAAADMFARVY-PSQPNLHGAYGNDLRL 226

RESULT 3
 AAB68435
 ID AAB68435 standard; protein; 227 AA.
 AC AAB68435;
 XX
 DT 23-JUN-2001 (first entry)
 XX
 DE Amino acid sequence of the floral homeotic protein PTD.
 XX
 KW Floral homeotic gene; PTD; PRLP; PTAG-1; PTAG-2; floral tissue; LEAFY;
 KW LFY; FLORICAULA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KW fertility; sterility.
 XX
 OS Populus balsamifera.
 OS
 PN CA2319853-A1.
 XX
 PD 01-APR-2001.
 XX
 PF 02-OCT-2000; 2000CA-02319853.
 XX
 PR 01-OCT-1999; 99US-00410464.
 XX
 PA (UDOR-) UNIV OREGON HEALTH SCI.
 PI Rottman WH, Straus SH, Brunner AM, Sheppard LA;
 XX
 DR WPI; 2001-336098/36.
 DR N-PSDB; AAF85391, AAF85392, AAF85393.
 XX
 PT Novel isolated polynucleotide derived from Populus species, useful for
 PT producing transgenic plants having modified fertility characteristic,

PT particularly sterility.

XX Claim 23; Page 43-44; 69pp; English.

CC The present sequence represents a floral homeotic protein, designated
CC PDF. It is derived from *Populus balsamifera* subsp. *trichocarpa*. The
CC specification also describes PRUF, PTAG-1 and PTAG-2 proteins. The floral
CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
CC LEAFY (LFY) and FLORICAULA (FLO), and is expressed in immature
CC inflorescences on which floral primordia are developing. PTD is a
CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
CC primordia from the onset of organogenesis. PTAG-1 and PTAG-2 are
CC homologues of AGAMOUS (AG). The floral homeotic proteins and
CC polynucleotides are useful for producing transgenic plants having
CC modified fertility characteristics, particularly sterility

XX Sequence 227 AA;

Query Match 51.9%; Score 611; DB 4; Length 227;

Best Local Similarity 55.2%; Pred. No. 2.7e-50; Mismatches 56; Indels 12; Gaps 4;

Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;

QY 1 MGRGKIEIKKIEPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60

QY 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
DB 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120

QY 121 LRGLEQTLBESLRIVNHRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 180
DB 121 LRGLEQTLBESLRIVNHRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 180

QY 121 LRGLEQHTMEALNGVGRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 179
DB 121 LRGLEQHTMEALNGVGRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 179

QY 181 VENQSRIVENSIPMVNECPQMFSPFRVYVHPO-----PNT-LGIGYSHDSL 226
DB 181 VENQSRIVENSIPMVNECPQMFSPFRVYVHPO-----PNT-LGIGYSHDSL 226

ABG30865 standard; protein; 227 AA.

AC ABG30865;

XX 29-AUG-2003 (revised)

XX 07-OCT-2002 (first entry)

DE Poplar protein transduction domain, PTD, protein.

XX Poplar; plant; DEFICIENS; transgenic; promoter;

KW protein transduction domain; floral homeotic gene;

KM floral-specific expression; cytotoxin; fertility; sterility; PTLF;

XX PTAG-1; PTAG-2.

OS *Populus balsamifera*; subsp. *trichocarpa*.

XX Key

XX Location/Qualifiers

XX 1.57

XX /label= "MADS domain

XX /note= "MADS is named for the first 4 proteins in which

XX it was discovered, yeast minichromosome maintenance

XX factor, floral homeotic genes AG and DEF and human serum

XX response factor"

XX 87.154

XX /label= K_domain

XX US6395892-B1.

XX 28-MAY-2002.

XX 01-OCT-1999; 99US-00410464.

PR 06-APR-1999; 98US-0080851P.

PR 06-APR-1999; 99US-00287700.

XX (UNOR-) UNIV OREGON HEALTH SCI.

XX Strauss SH, Rottmann W, Brunner A, Sheppard L;

XX N-PSDB; ABK88484, ABK88485.

XX WPI; 2002-572653/61.

XX disclosure; Col 39-42; 46pp; English.

XX The invention relates to an isolated nucleic acid molecule especially a

CC protein transduction domain (PTD) promoter: (i) that hybridizes under

CC wash conditions of 0.2 x SSC (saline sodium citrate), 0.1 %SDS (sodium

CC dodecyl sulphate) at 65 plus or to nucleotides or (ii) comprising 35

CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene

CC and is the homologue of DEFICIENS. Also includes are a recombinant

CC nucleic acid comprising the PTD promoter, a cell transformed with the

CC recombinant nucleic acid and a transgenic plant comprising the

CC expression of genes such as cytotoxins, that are employed in genetic

CC ablation strategies to produce trees having modified fertility

CC characteristics, including sterility. Genetic constructs comprising

CC antisense versions or dominant negative mutants of PTD are useful in

CC producing genetically engineered Poplars and other trees, and for sense

CC suppression. Also disclosed are 3 other homeotic genes PRUF, PTAG-1 and

CC PTAG-2 (none are defined). The present sequence is the PTD protein.

CC (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 227 AA;

Query Match 51.9%; Score 611; DB 5; Length 227;

Best Local Similarity 55.2%; Pred. No. 2.7e-50; Mismatches 56; Indels 12; Gaps 4;

Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;

QY 1 MGRGKIEIKKIEPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNRQVTYSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60

QY 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120
DB 61 STDIKGIYERYGVVNTGMDLMAQYERMONTLKHLNEINONLRKEIRRRKGEELGMDIKQ 120

QY 121 LRGLEQTLBESLRIVNHRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 180
DB 121 LRGLEQTLBESLRIVNHRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 180

QY 121 LRGLEQHTMEALNGVGRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 179
DB 121 LRGLEQHTMEALNGVGRKYNVATOTDPTKKYKLSKSTRETYRALLNELMKENPNYGFN 179

QY 181 VENQSRIVENSIPMVNECPQMFSPFRVYVHPO-----PNT-LGIGYSHDSL 226
DB 181 VENQSRIVENSIPMVNECPQMFSPFRVYVHPO-----PNT-LGIGYSHDSL 226

ABU61893 standard; protein; 227 AA.

XX ABU61893;

XX 18-AUG-2003 (first entry)

XX Poplar homeotic protein PTD.

XX Poplar; PTD; deficiens; homeotic gene; floral development; sterile tree;

XX pulp; paper; plant.

XX *Populus balsamifera* subsp. *trichocarpa*.

XX Key

XX Location/Qualifiers

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FT Domain 1..57
FT /label= MADS_domain
FT 87..154
FT /label= K_domain
XX US200303628-A1.
XX
XX 13-FEB-2003.
XX
XX 21-MAR-2002; 2002US-00104580.
XX
XX 06-APR-1998; 98US-0080851P.
XX 06-APR-1999; 98US-00287700.
XX 01-OCT-1999; 99US-00410464.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Strauss SH, Rottmann W, Brunner A, Sheppard L;
XX WPI, 2003-466273/44.
XX N-PSDB; ACA62517, ACA62518.
XX
XX New floral homeotic nucleic acid molecules, useful for the manipulation
XX of flowering in Poplar and other plant species, and for producing
XX transgenic plants having modified fertility characteristics, particularly
XX sterility.
XX
XX Claim 23; Page 22; 48pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising at
XX least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
XX 4 homeotic genes from poplar, PRUF (LEAFY and FLORICA homologue), PTD
XX (DEFICIENS homologue), and PRAG-1/PRAG-2 (both homologues of AGAMOUS).
XX Also included are a recombinant nucleic acid molecule comprising a
XX promoter sequence operably linked to the nucleic acid molecule, a cell
XX transformed with the nucleic acid molecule, a transgenic plant comprising
XX the recombinant nucleic acid molecule and the purified protein encoded
XX by the nucleic acids. The nucleic acid molecules are useful for the
XX manipulation of flowering in Poplar and other plant species, for
XX producing transgenic plants having modified fertility characteristics
XX (particularly sterility) and in the pulp and paper industries. The
XX present sequence is the poplar PTD protein
XX
XX SQ
XX
XX Sequence 227 AA;
XX
XX Query Match 51.9%; Score 611; DB 7; Length 227;
XX Best Local Similarity 55.2%; Pred. No. 2,7e-50;
XX Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;
XX
XX QY 1 MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX DB 1 MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX CC MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX CC MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX
XX QY 61 STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX DB 61 STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX CC STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX CC STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX
XX QY 121 LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX DB 121 LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX CC LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX CC LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX
XX QY 181 VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX DB 181 VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX CC VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX CC VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX
XX RESULT 6
XX AA58654
XX AA58654 standard; protein; 227 AA.
XX
XX AC AA58654;
XX
XX DT 11-APR-2000 (first entry)

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XX XX
XX DE Poplar PTD floral homeotic gene-encoded protein.
XX XX
XX KM Poplar; PTD; floral homeotic gene; transgenic plant; sterility;
XX XX
XX OS Populus balsamifera subsp. trichocarpa.
XX
XX FH Key
XX FT location/Qualifiers
XX FT 1..60
XX FT /note= "MADS domain"
XX FT Domain 68..143
XX FT /note= "K domain"
XX
XX PN CA2227940-A1.
XX
XX PD 06-OCT-1999.
XX
XX PF 07-APR-1998; 98CA-02227940.
XX
XX PR 06-APR-1998; 98US-00080851.
XX
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX PI Rottmann WH, Brunner AM, Sheppard LA, Strauss SH;
XX
XX DR WPI, 2000-106662/10.
XX
XX N-PSDB; AA257942, AA257943.
XX
XX PT Nucleic acid from Populus trichocarpa genes, useful for producing
XX transgenic plants, particularly trees, with modified fertility
XX characteristics such as sterility.
XX
XX PS Claim 31; Page 49-50; 92pp; English.
XX
XX XX
XX The present sequence is that of the novel PTD protein of poplar (Populus
XX balsamifera subsp. trichocarpa), as deduced from newly isolated PTD gene
XX and cDNA sequences (see AA257942-43). PTD is 1 of 4 novel floral homeotic
XX genes identified in this poplar species. It is a homologue of DEFICIENS
XX and is expressed strongly in stamen primordia from the onset of
XX organogenesis, and is also expressed at low levels in carpel primordia.
XX PTD contains both a MADS domain and a K-domain. The invention provides
XX nucleic acid sequences of the 4 novel Populus genes, the corresponding
XX cDNA sequences (see AA247942-45) and deduced amino acid sequences (see
XX AA58454-57). It also provides methods of using the gene and cDNA
XX sequences to produce genetically engineered Populus and other trees
XX having modified fertility characteristics, including sterility. Genetic
XX constructs useful in producing genetically engineered Populus and other
XX trees include antisense versions of PTD, dominant negative mutants, and
XX constructs useful for sense suppression. Sterile trees allow increased
XX wood yield and a reduction in the production of allergens such as pollen
XX
XX SQ
XX
XX Sequence 227 AA;
XX
XX Query Match 50.6%; Score 595; DB 3; Length 227;
XX Best Local Similarity 53.9%; Pred. No. 9.5e-49;
XX Matches 125; Conservative 37; Mismatches 58; Indels 12; Gaps 4;
XX
XX QY 1 MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX DB 1 MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX CC MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX CC MGRGKIEIKIENPTNROVYTSKRVRGILKKAKELTVLCDAQVSLIMFSGTGADYCSF 60
XX
XX QY 61 STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX DB 61 STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX CC STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX CC STDIKGIYERYOVTGMDLMAOYEROMNTLKLININONLKRERIRRRGEGELGMDIKQ 120
XX
XX QY 121 LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX DB 121 LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX CC LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX CC LRGLGQTLSESLIRVRRKXHVATQTDYKKKLSSTRETYALTHEIDMKEENPNYGFN 180
XX
XX QY 181 VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX DB 181 VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX CC VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX CC VENQSRIVENSIPMNVCECPMFSEFVHPNQ-----PNI-LGLGVESHDSL 226
XX
XX 180 VDN-----EAAVALANGASNLVAFRLHGHNNHNLRLPDLHLDGDFGAHELR 226

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RESULT 7

AAE25757

ID AAE25757 standard; protein; 227 AA.

XX AAE25757;

XX 04-NOV-2002. (first entry)

XX Soybean AP3 homologue protein from clone sflin.pk001.116.

XX Floral developmental protein; flowering locus T; APETALA3; transgenic;
 XX FT; AP3; transgenic plant; fertility; flower development; gene mapping;
 XX sterility; plant growth; inflorescence architecture; plant morphology;
 XX tissue culture; cell division; soybean.

XX Glycine max.

XX MO200244390-A2.

XX 06-JUN-2002.

XX 21-NOV-2001; 2001MO-US043750.

XX 28-NOV-2000; 2000US-0253415P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX Cahoon EB, Cahoon RE, Klein TM, Rafalski AJ, Sakai H;

XX WPI; 2002-547703/58.

XX N-PSDB; AAD42259.

XX New floral developmental polypeptide having flowering locus T or AP3
 XX homolog activity, useful for immunological screening of cDNA expression
 XX libraries.

XX Claim 17; Page 80-81; 88pp; English.

XX The present invention relates to novel floral developmental proteins,
 XX more specifically flowering locus T (FT) or APETALA3 (AP3) homologue
 XX proteins and polynucleotides encoding such proteins. Floral developmental
 XX polynucleotides are useful for transforming cells or for producing plants
 XX by transforming the plant cells with the polynucleotides and regenerating
 XX the plants from the transformed plant cells. Sequences of the invention
 XX are useful for immunological screening of cDNA expression libraries. They
 XX are also useful for creating transgenic plants. Polynucleotides of the
 XX invention are used as probes for genetically and physically mapping the
 XX genes that they are a part of and as markers for traits linked to those
 XX genes. AP3 homologues may be useful for engineering plant sterility or
 XX fertility, flower development and morphology. FT or TFL1 homologues are
 XX useful for engineering flowering time, plant growth rate, inflorescence
 XX architecture, tissue culture morphology and rate of cell division to
 XX enhance transformation. The present sequence is soybean AP3 homologue
 XX protein

SQ Sequence 227 AA;

Query Match 47.4%; Score 557.5; DB 5; Length 227;

Best Local Similarity 51.2%; Pred. No. 3.9e-45; Indels 3; Gaps 3;

Matches 109; Conservative 42; Mismatches 59; Indels 3; Gaps 3;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

DB 1 MARGKIQIKRIENNTROVTSKRRNGLFKKANELTVLCDAKYSIMFSSTGLADYCSF 60

QY 61 STDIKGIYERYQVVTGMDLNNAYERMONTLKLHNEINONLRKEIRRRKEELEGMDIKQ 120

DB 61 STSTKQFPDQYQVTLGVDLNNSHYENQENIKKLKEVNRNLRRKEIRRRKEELEGMDIKQ 120

QY 121 LRGLEQTLSESLRIYHRKYHVAATQDTYKKKLKSTRETYRALLHLELDMKEENPNYGFN 180

DB 121 LKLEBEMDKAAKVVERKRYKVTITQIDQRKKFNKEVHNRLLHLDLQAKADPRFAL- 179

QY 181 VENQSRITYENSIPMNECPQMFSEFRVHNPQN 213

DB 180 IDNGGE-YESVIGFNSLGPMEFALS-IQPSHPS 210

RESULT 8

AAR43385

ID AAR43385 standard; protein; 231 AA.

XX AAR43385;

XX 25-MAR-2003 (revised)

XX 19-JUN-1994 (first entry)

XX Product of homeotic gene green petal.

XX Plant; organ morphogenesis; control; petunia; petals.

XX Petunia.

XX MO9321322-A1.

XX 28-OCT-1993.

XX 13-APR-1993; 93MO-US003508.

XX 13-APR-1992; 92US-00867580.

XX 06-JUL-1992; 92US-00909589.

XX (UYRQ) UNIV ROCKEFELLER.

XX Halfter U, Van Der Krol AR, Kush A, Chua N;

XX WPI; 1993-351732/44.

XX N-PSDB; AAO51189.

XX Plant organ morphogenesis control and determ. - by regulating the
 XX expression of homeotic genes which determine the identity of the organ.

XX Disclosure; Fig 2; 74pp; English.

XX The homeotic gene green petal from petunia has been cloned and
 XX characterised previously. The gene was used in a new method for
 XX controlling the morphogenesis of plant organs comprising regulating the
 XX expression of the gene using ectopic expression. Such a method can be
 XX used to determine and control plant organ morphogenesis, such as
 XX modifying petals without altering the reproductive portions of the
 XX flower. See also AAR43386-7. (Updated on 25-MAR-2003 to correct FN
 XX field.)

SQ Sequence 231 AA;

Query Match 44.9%; Score 528; DB 2; Length 231;

Best Local Similarity 48.8%; Pred. No. 2.8e-42; Indels 6; Gaps 3;

Matches 105; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60

DB 1 MARGKIQIKRIENNTROVTSKRRNGLFKKANELTVLCDAKYSIMFSSTGLADYCSF 60

QY 61 STDIKGIYERYQVVTGMDLNNAYERMONTLKLHNEINONLRKEIRRRKEELEGMDIKQ 120

DB 61 SITTKQLFDLYQVTVGVDLNNSHYEQQLRKLKEVNRNLRRKEIRRRKEELEGMDIKQ 120

QY 121 LRGLEQTLSESLRIYHRKYHVAATQDTYKKKLKSTRETYRALLHLELDMKEENPNYGFN 180

DB 121 LEELENNVNSLILRRERYKVIANGIETFKKKVRVVEIHRNLLLEFARQEDP--YG 177

QY 181 VENQSRITYENSIPMNECPQMFSEFRVHNP--QPN 213

DB 178 LVEQBGDYNVSLGFRNGHRIALR--LQPNHNP 211

PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
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Query Match 43.3%; Score 509.5; DB 3; length 232;
Best Local Similarity 47.8%; Pred. No. 1.7e-40;

Matches .107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

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Dd 61 NTTKKEIVDLYDTISDVWVAQYEMOEFTKERKLETNNAQLTOIKRLGCDELDEIDIE 120

OY 121 LRIGEOFLTESLRIVHRKYHVIATOTDYRKKLKSTRETYRALIHEDLMKENPNYNGN 180

Dd 121 LRRLEDMENTFVLVERKFSLGNQILETTKKRNKSODDLOKNILHELELRADPHYG- 179

OY 181 VENOSRIYENSIPMWECPOMFSPRVVHPNPMLLGYESHDJ 224

Dd 180 VDNCGD-YDSVVGYOIESGRAYALR-FHQNHNY----YNHGCL 217

RESULT 11
ADO61551 standard; protein, 232 AA.

AC ADO61551;
XX XX
DT 15-JUL-2004 (first entry)
DE Transcription factor GI33, SEQ ID 18.
KM Plant; transcription factor; transgenic plant; abiotic stress tolerance;
KM osmotic stress tolerance; cold tolerance; heat tolerance;
KW low nitrogen tolerance; low phosphate tolerance; fungal disease;
XX glycosylate resistance; flowering; fertility; seed development.
Arabidopsis thaliana.

PX W02004031349-A2.
PD 15-APR-2004.
XX XX
PF 18-SEP-2003; 2003WO-US030292.
PR 18-SEP-2002; 2002US-0411937P.
PR 17-DEC-2002; 2002US-043416P.
PR 24-APR-2003; 2003US-0465809P.
XX XX
PA (MENDEL) MENDEL BIOTECHNOLOGY INC.
PI Jiang C, Heard JE, Ratcliffe O, Creelman RA, Adam LD, Reuber TJ,
RX Richmann JF, Haake V, Dubell AM, Keddie JS, Sherman BK,
DX WP1, 2004-330163/30.
DR N-PDB; ADO61550.
PS New recombinant polynucleotide encoding transcription factor
PT polyepitides, useful for producing transgenic plants with advantageous
XX properties compared to a reference plant.
Disclousure; SEQ ID NO 18; 510pp; English.

The present invention relates to novel plant transcription factor
CC proteins (I) and nucleotide sequences (II) (ADO61534-ADO61778). The
CC sequences can be used to produce transgenic plants. (III), where the transgenic plant has an altered trait as compared to a
CC non-transgenic plant or wild-type plant. The transgenic plant comprises
CC an altered trait selected from increased tolerance to abiotic stresses,
CC increased germination in cold, increased tolerance to freezing conditions,
CC increased tolerance to osmotic stress, increased tolerance to salt, increased
CC germination in heat, increased tolerance to drought, increased
CC increased tolerance to low nitrogen conditions, increased tolerance to
CC low phosphate conditions, increased tolerance to disease, including
CC fungal diseases and particularly Erysiphe, Fusarium and Botrytis
CC increased tolerance to multiple fungal pathogens, increased resistance to

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PR 05-OCT-1999; 99US-0157753P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 43.3%; Score 509.5; DB 3; Length 241;
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DB 10 MARGKIQIKRIEIQNRQVYSKRRNGLFKKAKELTVLCDAQVSLMFSSNKLHETISP 69
QY 61 STDIKIYERYQVVTGMDLMAQYERQNTLKLHNEINQNLKRIERRKGELEGMIDIKQ 120
DB 70 NTTKTEIVDLYQISVDVMAQYERMQETKRLLETNNLRQIQKRLGEGCDELIDIOE 129
QY 121 LRGLQOTLEBSLRIVHRKRYHVIATOTDYKKKKLSTRETFRALIHEDMKENPNYGFN 180
DB 130 LRRLDEMENTFALVERKFKSLGNQIETTKKKKNSQOIQKVLHLELRADPHYGL- 188
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DB 189 YDSVGD-YDSVLGYQIEGSRAYALR-FHONHHY---YPNHGL 226

RESULT 14
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XX AAG25577;
AC
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29698.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridization assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.

XX EN EPI033405-A2.
XX PD
XX XX 06-SEP-2000.
PF XX 25-FEB-2000; 2000EP-00301439.
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PR 15-SEP-1999; 99US-0154018P.

PR 16-SEP-1999; 99US-0154039P.
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PR 05-OCT-1999; 99US-0157753P.
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PR 08-OCT-1999; 99US-0158232P.
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Query Match 43.1%; Score 507.5; DB 3; Length 232;

Best Local Similarity 47.8%; Pred. No. 2.7e-40; Matches 107; Conservative 45; Mismatches 65; Indels 7; Gaps 4;

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QY 61 STDIKQIERYQVVTGMNLNNAQYBERMONTLKHLINEINONLRKEIRRKGELEGDIXO 120
DB 61 NNTTKELIVDLQYITSDVDWATQYERMQETKRLLEFNRLRQIQKQRLGEGCLNKLDIOE 120
QY 121 LRGLLETTLESRLIYHRRKRVHATQTDYTKKKLXSTREYRRLIHELMKENPNYGFN 180
DB 121 LRLLEEMERTFLVYERKFKSLGNQIETTKKKNKSQODIQKXLIHELELRADPHYGL- 179
QY 181 VENQSRIVENSIPMWNCEPQMFSPFRVVPNPQLLGLGYESHDL 224
DB 180 VDNQGD-YDSVLQYIEGSHAYALR-FHQNHVHY---YFNHGL 217

RESULT 15

AAAG25576
ID AAAG25576 standard; protein; 242 AA.

XX AAAG25576;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 29697.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-00301439.

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Query Match 43.1%; Score 507.5; DB 3; Length 242;
Best Local Similarity 47.8%; Pred. No. 2.8e-40;
Matches 107; Conservative 45; Mismatches 65; Indels 7; Gaps 4;

QY 1 MGRGKLEIKIENPNNROVTVSKRRVGIKKAKELTVLCDAOVSLMFSTGKLADYCSG 60
DB 11 MGRGKIQIKRIENQNNROVTVSKRRNGLPFKKAHETVLCDAVSLTFSSNNLHETYS 70
QY 61 STDINGIERYQVATGMDLWMAOYERMONTKLHNEINONLREKIRRRGEELEGMDIQ 120
DB 71 NTKKEIVDLQYISDVDAVATQYERMOETKRLTNTNRLTQIKORLGECCLNKLDIOE 130
QY 121 LRGEQTLBESLRVRRKRYHVATQTDYVKKKLTSTREYALTHEIDMKENNYGN 180
DB 131 LRLEDEMENTFKLVBERKFKSLGNQIETTKKKNSQODIQKNLHETELRAEDPHYGL- 189
QY 181 VENQSRITYENSIPMVAECPOMSFRVYHNPONLGLGYESHDL 224
DB 190 VDNQGD-YDSVLGYQYEGSRAYALR-FHONHHY----YPNHGL 227

Search completed: January 27, 2005, 13:18:10
Job time : 162 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 13:12:19 ; Search time 41 Seconds
(without alignments)
532.712 Million cell updates/sec

Title: US-10-690-246-2

Perfect score: 1177
Sequence: 1 MGRGKLEIKKINPTNRQVT.....HPNQVNLGLGYESHDLSLA 227

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	46.8	222	2 S23731	MADS box protein T
2	546	46.4	229	2 T09335	MADS-box protein N
3	533	45.3	227	2 S12378	MADS box protein d
4	528	44.9	231	2 S31693	MADS box protein g
5	515.5	43.8	228	2 T07066	MADS-box protein h
6	512.5	43.5	228	2 T07410	MADS box protein h
7	509.5	43.3	232	2 A42095	floral homeotic pr
8	503.5	42.8	224	2 T14473	MADS box protein 2
9	493.5	41.9	224	2 T10715	MADS-box protein c
10	488.5	41.5	224	2 T14474	MADS box protein c
11	405.5	34.5	203	2 T06277	MADS box protein a
12	400	34.0	208	2 A53839	B function floral
13	391	33.2	212	2 S31707	floral homeotic pr
14	387.5	32.8	209	2 S35226	homeotic protein g
15	386	32.8	212	2 S60286	PP3 protein - gar
16	385	32.7	210	2 T01689	floral binding pro
17	382.5	32.5	209	2 T03894	MADS box protein -
18	381.5	32.4	215	2 S28062	homeotic protein g
19	377	32.0	210	2 T03902	MADS box protein
20	327	27.8	234	2 T52100	MADS-box transcrip
21	323	27.4	251	2 T14456	MADS box protein h
22	320.5	27.2	252	2 F39534	floral homeotic pr
23	320	27.2	273	2 T03410	MADS box protein -
24	319	27.1	248	2 T07185	floral homeotic pr
25	318	27.0	248	2 B39534	MADS box protein A
26	317.5	27.0	253	2 S57586	MADS-box regulator
27	317	26.9	234	2 A84515	probable MADS-box
28	316.5	26.9	229	2 T08040	MADS-box protein -
29	316	26.8	250	2 T04167	MADS box protein -

30	316	26.8	252	2 A43484	probable transcrip
31	315	26.8	262	2 T51409	MADS box protein A
32	314.5	26.7	254	2 S52236	MADS box protein a
33	314	26.7	256	2 S27109	MADS box protein M
34	310.5	26.4	245	2 T09569	MADS box protein M
35	309.5	26.3	256	2 T45817	MADS transcription
36	309.5	26.3	284	2 T05033	floral homeotic pr
37	309.5	26.3	284	2 A85214	floral homeotic pr
38	308.5	26.2	250	2 D39534	MADS box protein A
39	308	26.2	248	2 T03592	floral homeotic pr
40	307.5	26.1	242	2 JQ2212	PMADS3 protein - g
41	307.5	26.1	246	2 E39534	floral homeotic pr
42	307.5	26.1	258	2 G84658	floral homeodomain
43	307	26.1	150	2 T14457	MADS box protein h
44	306	26.0	227	2 H84614	probable MADS-box
45	306	26.0	248	2 S20886	MADS box protein s

ALIGNMENTS

RESULT 1
S23731
MADS box protein TDR6 - tomato (fragment)
N/Alternate names: floral homeotic protein TM6
C/Species: Lycopersicon esculentum (tomato)
C/Date: 27-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S23731; S38778
R/Punell, L.; Abu-Abeid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E.
Plant J. 1, 255-266, 1991
A/Title: The MADS box gene family in tomato: temporal expression during floral development
A/Reference number: S23728; MUID:93251098; PMID:1688249
A/Accession: S23731
A/Molecule type: mRNA
A/Residues: 1-222 <PNU>
A/Cross-references: UNIPROT:Q40171; EMBL:X60759
R/Punell, L. the EMBL Data Library, July 1991
A/Reference number: S38778
A/Accession: S38778
A/Molecule type: mRNA
A/Residues: 1-159, 'T', 161-222 <PNU>
A/Cross-references: EMBL:X60759; NID:919385; PID:919386
C/Genetic:
A/Map position: 2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homolc
C/Keywords: DNA binding; nucleus; transcription regulation
F/1-54/Domain: serum response factor DNA-binding domain homology (fragment) <SRF>

Query Match 46.8%; Score 551; DB 2; Length 222;
Best Local Similarity 50.4%; Pred. No. 4.3e-32;
Matches 114; Conservative 41; Mismatches 65; Indels 6; Gaps 4;

QY 4 GKIEIKKINPTNRQVTYSKRGVILKKELVLDQAVSLMFSSTGLADYCSPTD 63
DB 1 GKIEIKKINPTNRQVTYSKRGVILKKELVLDQAVSLMFSSTGLADYCSPTD 60
QY 64 IKGIYERQVVTQMDLMNAQYERQNTLKLHNEINONLRKEIRRRKGELEGDKQLRG 123
DB 61 TKKMDIQYQALGDVIMSHYKMGQENIKRLKINNKLRREITHRGEDMGSLDELCH 120
QY 124 LEQTELESLRIVHRKRYVIAATOTDYKKKLSKSTRETRALVHEDMKENPNYGRVEN 183
DB 121 LQENITEVSVAIERKRYHYVKNQTDCKKARVLEQNGNLVLDLBAKCDPRXYV-VEN 179
QY 184 OSRIYENSIPMVNECPQWFSFRV--VHPNPNLGLGYESHDLSLA 227
DB 180 EGH-YHSVAVFANGVNHVYFRLOPHNPLQNGGFG--SRDLRLS 222

RESULT 2
T09335
MADS-box protein NMH 7 - alfalfa

C/Species: Medicago sativa (alfalfa)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09335
R/Kirby, C.; Heard, J.; Carroll, S.; Leshner, J.; Gantner, G.; Dunn, K.
submitted to the EMBL Data Library, January 1998
A/Reference number: 216647
A/Accession: T09335
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-229 <KIR>
A/Cross-references: UNIPROT:O49173; EMBL:AF042068; NID:g2827299; PID:g2827300
A/Experimental source: Strain Iroquois; root nodules
C/Genetics:
A/Genes: nmh 7
A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 46.4%; Score 546; DB 2; Length 229;
Best Local Similarity 50.7%; Pred. No. 1e-31;
Matches 109; Conservative 38; Mismatches 64; Indels 4; Gaps 2;

QY 1 MGRGKIEIKKTEPNTNROVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
Db 1 MARGKIQIKRIENNTNROVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
QY 61 STDIKGIYERYOAVTGMDLMAQYERMQNTLKHLEINONLRKEIRRRGGELEGMIDIKQ 120
Db 61 SASTKQFPDQYKAVGVGLDMSHYEKMQLKLDVNRNLRKEIRRRGGELEGMIDIKQ 120
QY 121 LRGLQTLRESLRIVRKHVYATOTDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
Db 121 LRLLEMDMSLKLIRKRYKVIQIDTORKKSNREVRNRLRLDADAEPR--FE 178
QY 181 VENQSRIVYENSIPWNECPQMF--SFRVYHNPQN 213
Db 179 NMDNGEYESVIGFNSLGRPMFALSLQTHNPN 213

RESULT 3

S12378

MADS box protein defA-1 - garden snapdragon
N/Alternate names: gene deficiencies protein
C/Species: Antirrhinum majus (garden snapdragon)
C/Date: 21-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S12378; S19232
R/Schwarz-Sommer, Z.; Hne, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Leemig,
EMBO J. 9, 605-613, 1990
A/Title: Deficiens, a homeotic gene involved in the control of flower morphogenesis in A
A/Reference number: S12378; MUID:9018395; PMID:1968830
A/Accession: S12378

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-227 <SOM>
A/Cross-references: UNIPROT:P23706; GB:X52023; NID:g16019; PIDN:CAA36268.1; PID:g16020
R/Schwarz-Sommer, Z.; Hne, I.; Huijser, P.; Flor, P.J.; Hansen, R.; Leemig,
EMBO J. 11, 251-263, 1992
A/Title: Characterization of the Antirrhinum floral homeotic MADS-box gene deficiencies: ex
A/Reference number: S19232; MUID:9215516; PMID:1346760
A/Accession: S19232
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-227 <SCH>
A/Cross-references: EMBL:X62810; NID:g16017; PIDN:CAA44629.1; PID:g16018
A/Genes: deficiens
A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match

45.3%; Score 533; DB 2; Length 227;

Best Local Similarity 48.6%; Pred. No. 8.3e-31;
Matches 104; Conservative 48; Mismatches 60; Indels 2; Gaps 2;

QY 1 MGRGKIEIKKTEPNTNROVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
Db 1 MARGKIQIKRIENNTNROVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
QY 61 STDIKGIYERYOAVTGMDLMAQYERMQNTLKHLEINONLRKEIRRRGGELEGMIDIKQ 120
Db 61 SASTKQFPDQYKAVGVGLDMSHYEKMQLKLDVNRNLRKEIRRRGGELEGMIDIKQ 120
QY 121 LRGLQTLRESLRIVRKHVYATOTDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
Db 121 LRLLEMDMSLKLIRKRYKVIQIDTORKKSNREVRNRLRLDADAEPR--FE 178
QY 181 VENQSRIVYENSIPWNECPQMF--SFRVYHNPQN 214
Db 180 VDNEDG-VNSVLGFPNGGPRITALRLPTNHHPTL 212

RESULT 4

S31693

MADS box protein gp - garden petunia
N/Alternate names: floral homeotic protein gp; transcription factor gp
C/Species: Petunia x hybrida (garden petunia)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S31693
R/Kush, A.; Brunelle, A.; Shavell, D.; Chua, N.H.
submitted to the EMBL Data Library, November 1992
A/Description: Nucleotide sequence and expression pattern of two genes encoding MADS bo:
A/Reference number: S31693
A/Accession: S31693
A/Molecule type: mRNA
A/Residues: 1-231 <KUS>
A/Cross-references: UNIPROT:O07472; EMBL:X69946; NID:g22664; PID:g22665
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 44.9%; Score 528; DB 2; Length 231;
Best Local Similarity 48.8%; Pred. No. 1.9e-30;
Matches 105; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

QY 1 MGRGKIEIKKTEPNTNROVYTSKRKRGILKKAKELTVLCDAQVSLIMFSTGKLADYCSF 60
Db 1 MARGKIQIKRIENNTNROVYTSKRKRGILKKAKELTVLCDAKVSIMFSTGKLHEYISF 60
QY 61 STDIKGIYERYOAVTGMDLMAQYERMQNTLKHLEINONLRKEIRRRGGELEGMIDIKQ 120
Db 61 SASTKQFPDQYKAVGVGLDMSHYEKMQLKLDVNRNLRKEIRRRGGELEGMIDIKQ 120
QY 121 LRGLQTLRESLRIVRKHVYATOTDTYKKKLKSTRETYRALIHELDMEKNPNYGFN 180
Db 121 LRLLEMDMSLKLIRKRYKVIQIDTORKKSNREVRNRLRLDADAEPR--FE 178
QY 181 VENQSRIVYENSIPWNECPQMF--SFRVYHNPQN 213
Db 178 LVEQEGDYNSVLGFPNGGPRITALRLPTNHHPTL 211

RESULT 5

T07066

MADS-box protein homolog DefA - potato
N/Alternate names: deficiencies analogue
C/Species: Solanum tuberosum (potato)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T07066
R/Garcia-Maroto, F.; Salami, F.; Rohde, W.
Plant J. 4, 771-780, 1993
A/Title: Molecular cloning and expression patterns of three alleles of the Deficiens-hom
A/Reference number: Z15896; MUID:94100991; PMID:77903890
A/Accession: T07066
A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

A:Molecule type: DNA
A:Residues: 1-228 <GAR>
A:Cross-references: UNIPROT:Q41417; EMBL:X67511; NID:G431225; PIDN:CAA47846.1; PID:G4312
A:Experimental source: cv. Granola; leaf
C:Genetics:
A:Gene: def4
A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
C:Superfamily: transcription factor equa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.8%; Score 515.5; DB 2; Length 228;
Best Local Similarity 52.7%; Pred. No. 1.5e-29;
Matches 97; Conservative 39; Mismatches 47; Indels 1; Gaps 1;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKKIENQTNQVTSKRRNGLFKKANELTVLCDAKVSIVMISSTGKLHEFISP 60
QY 61 STIKIGYERYQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
DB 61 SITTKQLFDLYQKTIQVDTSHYERKQEQDLRKLDVNRMLRKEIRQRMGESLNDLNFQ 120
QY 121 LRGLQETLESRLIVRRKXHVATQTDYTKKKLSTRETYRALIHELDMKEENPNYGFN 180
DB 121 LRLLEMEVNDLSKLIRKRYVIGNQIETRYKKVNVBEIHRNLLLEFDARQEDP-YGGL 179
QY 181 VENQ 184
DB 180 VEQE 183

RESULT 6
T07410
MADS box protein homolog DEF2 - potato
N:Alternate names: deficiens analogo
C:Species: Solanum tuberosum (potato)
C>Date: 14-May-1999 #sequence-revision 14-May-1999 #text-change 09-Jul-2004
C:Accession: T07410
R:Garcia-Maroto, F.
submitted to the EMBL Data Library, August 1992
A:Reference number: Z16019
A:Accession: T07410
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-228 <GAR>
A:Cross-references: UNIPROT:Q41477; EMBL:X67508; NID:G511064; PIDN:CAA47845.1; PID:G5110
C:Experimental source: cv. H81.1506/60; dev. stage vegetative; tissue type flower
C:Genetics:
A:Gene: def2
C:Superfamily: transcription factor equa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.5%; Score 512.5; DB 2; Length 228;
Best Local Similarity 52.2%; Pred. No. 2.4e-29;
Matches 96; Conservative 39; Mismatches 48; Indels 1; Gaps 1;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKKIENQTNQVTSKRRNGLFKKANELTVLCDAKVSIVMISSTGKLHEFISP 60
QY 61 STIKIGYERYQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
DB 61 SITTKQLFDLYQKTIQVDTSHYERKQEQDLRKLDVNRMLRKEIRQRMGESLNDLNFQ 120
QY 121 LRGLQETLESRLIVRRKXHVATQTDYTKKKLSTRETYRALIHELDMKEENPNYGFN 180
DB 121 LRLLEMEVNDLSKLIRKRYVIGNQIETRYKKVNVBEIHRNLLLEFDARQEDP-YGGL 179
QY 181 VENQ 184
DB 180 VEQE 183

RESULT 7
A42095
floral homeotic protein APETALA3 (AP3) - Arabidopsis thaliana
N:Alternate names: homeotic protein APETALA3; MADS-box regulatory protein AP3
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Mar-1993 #sequence-revision 18-Nov-1994 #text-change 09-Jul-2004
C:Accession: A42095; S52633; T47593
R:Jack, T.; Brockman, L.L.; Meyerowitz, E.M.
Cell 68, 683-697, 1992
A:Title: The homeotic gene APETALA3 of Arabidopsis thaliana encodes a MADS box and is ex
A:Reference number: A42095; MUID:92154682; PMID:1346756
A:Accession: A42095
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <UAC>
A:Cross-references: UNIPROT:P35632; GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A:Experimental source: petals, stems
A:Note: sequence extracted from NCBI backbone (NCBIN:82520, NCBI:P:82521)
R:Okamoto, H.; Yano, A.; Shirahashi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid
A:Reference number: S52633; MUID:95036018; PMID:7948893
A:Accession: S52633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-63 <OKA>
A:Cross-references: GB:D21125
R:Biocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quettier, F.; Salanoubat M.Mewes,
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24469
A:Accession: T47593
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <BLO>
A:Cross-references: EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Genetics:
A:Map position: 3
A:Insertions: 63/2; 85/3; 106/2; 139/3; 153/3; 168/3
A:Note: T12E18.30
C:Superfamily: transcription factor equa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match 43.3%; Score 509.5; DB 2; Length 232;
Best Local Similarity 47.8%; Pred. No. 3.9e-29;
Matches 107; Conservative 46; Mismatches 64; Indels 7; Gaps 4;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MARGKIQIKKIENQTNQVTSKRRNGLFKKAKELTVLCDAKVSIVMISSTGKLHEFISP 60
QY 61 STIKIGYERYQVVTGMDLMAQYERQNTLKLHNEINQNLKREIRRKKEELGMDIKQ 120
DB 61 SITTKQLFDLYQKTIQVDTSHYERKQEQDLRKLDVNRMLRKEIRQRMGESLNDLNFQ 120
QY 121 LRGLQETLESRLIVRRKXHVATQTDYTKKKLSTRETYRALIHELDMKEENPNYGFN 180
DB 121 LRLLEMEVNDLSKLIRKRYVIGNQIETRYKKVNVBEIHRNLLLEFDARQEDP-YGGL 179
QY 181 VENQ 184
DB 180 VEQE 183

RESULT 8
T14473
MADS box protein ZAP3 - broccoli
N:Alternate names: homeotic protein ZAP3
C:Species: Brassica oleracea var. botrytis (broccoli)
C>Date: 20-Sep-1999 #sequence-revision 20-Sep-1999 #text-change 09-Jul-2004

C/Accession: T14473
R/Carr, S.M.; Irish, V.F.
Planta 201, 179-188, 1997
A/Title: Floral homeotic gene expression defines developmental arrest stages in *Brassica*
A/Reference number: Z18110; MUID:97237761; PMID:9084216
A/Accession: T14473
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-224 <CAR>
A/Cross-references: UNIPROT:Q96359; EMBL:U67455; NID:g1561785; PID:g1561786
A/Experimental source: variety *italica*; flower
C/Genetics:
A/Gene: 2AP3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 42.8%; Score 503.5; DB 2; Length 224;
Matches 101; Conservative 41; Mismatches 47; Indels 11; Gaps 2;

```
Qy 1 MGRGKIEIKIENPTNRQVYTKRRVGIKKAKELTVLCDAVSLIMFSSSTGKLADYCSF 60
Db 1 MGRGKIQIKRIENQTNQVYTKRRNGLFKKAHELTVLCDAVSLIMFSSSNKLFHFISF 60
Qy 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKKEIRRRKGEELGMDIQ 120
Db 61 NTKTKELIDLYQVSDVDVWNAHYERMOETKRLKLETRNLFTQIKQRLGECLEDFDIOE 120
Qy 121 LRGLQTLBESLRIVRRKHVIAVATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
Db 121 LLSLEEMENFTKLVYERKFKSLGNQETTKKKKNSQODIQKLLHLELRABDPHYGL- 179
Qy 181 VEN-----QSRIYEN 190
Db 180 VDNCGDYDSVLGYQLRPHQN 199
```

RESULT 9
T10715
MADS-box protein CMB2 - clove pink
C/Species: *Dianthus caryophyllus* (clove pink)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10715
R/Baudinette, S.C.; Savin, K.W.
Submitted to the EMBL Data Library, March 1995
A/Description: Carnation MADS box genes.
A/Reference number: Z17094
A/Accession: T10715
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-214 <BAU>
A/Cross-references: UNIPROT:Q42498; EMBL:L40405; NID:g695318; PID:g695319
A/Experimental source: cv. *Scania*; petals
C/Genetics:
A/Gene: CMB2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; transcription factor; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 41.9%; Score 493.5; DB 2; Length 214;
Matches 97; Conservative 36; Mismatches 55; Indels 1; Gaps 1;

```
Qy 1 MGRGKIEIKIENPTNRQVYTKRRVGIKKAKELTVLCDAVSLIMFSSSTGKLADYCSF 60
Db 1 MGRGKIEIKRIENQTNQVYTKRRNGLFKKAHELTVLCDAVSLIMFSSSNKLFHFISF 60
Qy 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKKEIRRRKGEELGMDIQ 120
Db 61 GVSLLKQMDVQKIGVLMKQWRQEOHRKYLFLNLSLRREISRRMGCDJEGTLIVE 120
Qy 121 LRGLQTLBESLRIVRRKHVIAVATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
```

```
Db 121 LSLQDEMEBAITQIRNKKYTKIKQTGTTRKIKNLERTITLDMELKFKGPOPAIG 180
Qy 181 VENQSRIVE 189
Db 181 -EDDPNRYE 188
```

RESULT 10
T14474
MADS box protein ap3 - broccoli
N/Alternate names: homeotic protein ap3
C/Species: *Brassica oleracea* var. *botrytis* (broccoli)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14474
R/Carr, S.M.; Irish, V.F.
Planta 201, 179-188, 1997
A/Title: Floral homeotic gene expression defines developmental arrest stages in *Brassica*
A/Reference number: Z18110; MUID:97237761; PMID:9084216
A/Accession: T14474
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-224 <CAR>
A/Cross-references: UNIPROT:Q96359; EMBL:U67456; NID:g1621332; PID:g1621333
A/Experimental source: flower
C/Genetics:
A/Gene: AP3
A/Intons: 63/2, 85/3, 106/2, 139/3, 153/2, 168/3
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 41.5%; Score 488.5; DB 2; Length 224;
Matches 98; Conservative 42; Mismatches 49; Indels 11; Gaps 2;

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Qy 1 MGRGKIEIKIENPTNRQVYTKRRVGIKKAKELTVLCDAVSLIMFSSSTGKLADYCSF 60
Db 1 MGRGKIQIKRIENQTNQVYTKRRNGLFKKAHELTVLCDAVSLIMFSSSNKLFHFISF 60
Qy 61 STDIGIYERYOVVGMGLMNAOYERMOYNTLKHLEINQNLKKEIRRRKGEELGMDIQ 120
Db 61 NTKTKELIDLYQVSDVDVWNAHYERMOETKRLKLETRNLFTQIKQRLGECLEDFDIOE 120
Qy 121 LRGLQTLBESLRIVRRKHVIAVATQDTYKKKLKSTREYRALIHLEMDKEENPNYGFN 180
Db 121 LLSLEEMENFTKLVYERKFKSLGNQETTKKKKTRASTKYKGLIHLELRABDPHYGL- 179
Qy 181 VEN-----QSRIYEN 190
Db 180 VDNCGDYDSVLGYQLRPHQN 199
```

RESULT 11
T06277
MADS box protein AP3 - tomato (fragment)
C/Species: *Lycopersicon esculentum* (tomato)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06277
R/Kramer, E.M.; Dorit, R.L.; Irish, V.F.
Genetics 149, 765-783, 1998
A/Title: Molecular evolution of genes controlling petal and stamen development: duplicati
A/Accession: T06277
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-203 <KRA>
A/Cross-references: UNIPROT:Q65135; EMBL:AF052868; NID:g3170489; PID:AA042583.1; PID:g31
A/Experimental source: strain *Celebrity*
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
Query Match
34.5%; Score 405.5; DB 2; Length 203;

C;Accession: S60288
R;Angenent, G.C.; Franken, J.; Buscher, M.; Weiss, D.; van Tunen, A.J.
Plant J. 5, 33-44, 1994
A;Title: Co-suppression of the petunia homeotic gene fbp2 affects the identity of the ge
A;Reference number: S60288; MID:94177174; PMID:7907515
A;Accession: S60288
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-212 <ANG>
A;Cross-references: UNIPROT:Q40883; EMBL:X71417; NID:9454264; PIDN:CA50549.1; PID:94542
C;Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match
Best Local Similarity 32.8%; Score 386; DB 2; Length 212;
Matches 87; Conservative 45; Mismatches 75; Indels 8; Gaps 5;

QY 1 MGRGKIEIKKTENPTNRQVYTSKRVRGILKKAKELTVLCDQVSLWFSSTGKLADYCS 60
Db 1 MGRGKIEIKRIENSSNRQVYTSKRVRGILKKAKELTVLCDQVSLWFSSTGKLADYCS 60
QY 61 STDIGIYERYQVVTGMDLMAOYERMONTLKLHNEINONLRKEIRRRKGEBLEGMDIKQ 120
Db 61 STTLPDMDGYQKTSGRIMDAKHENLSNEIDRIKKENDSMQVKLRHLKGEDINSINKE 120
QY 121 LRGLQTLBESLRIVRKRKYHVIATQDTYKKKLKSTRETYRALIHEDMKREENPNYGN 180
Db 121 LMTVEBGLTNGLSISAKOSEILR---IVRKNQDILEEHKQLOVALHQR-ENAMAGN 175
QY 181 VENOSRIYENSIPWNECPQM-PSFRVHNPONL 214
Db 176 RMWIEEYVHOR-DRDYEYQOMPALR-VQPMQPNL 208

Search completed: January 27, 2005, 13:22:13
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:04:28 ; Search time 193 Seconds

(without alignments)
676.736 Million cell updates/sec

Title: US-10-690-246-2

Sequence: 1 MGRGKIEIKIENPTNRQVY.....HPNPVLGLGIESHDLSTA 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot 02: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	69.7	225	2	084M23
2	782.5	66.5	228	2	08LTI0
3	781.5	66.4	228	2	08LRS9
4	738	62.1	221	2	09FRI2
5	730.5	62.1	228	2	084M22
6	716	60.8	234	2	084M24
7	701.5	59.6	231	2	084M21
8	700	59.5	200	2	09LJ99
9	684.5	58.2	224	2	09XU65
10	680.5	57.8	224	2	0944S9
11	675	57.3	227	2	09M6N9
12	664	56.4	223	2	09ZPM9
13	663	56.3	222	2	06CHI3
14	663	56.3	232	2	06CHI3
15	653	55.5	229	2	AA848126
16	651.5	55.4	214	2	082130
17	642	54.5	227	2	0948U8
18	642	54.5	227	2	076DP7
19	638.5	54.2	219	2	BA015367
20	638.5	54.2	219	2	06TH79
21	630.5	53.6	228	2	AA06664
22	611	51.9	227	2	065141
23	600.5	51.0	228	2	065211
24	588	50.0	179	2	06GW2
25	588	50.0	179	2	070J07
26	582	49.4	225	2	CA853898
27	579	49.2	204	2	06GW3
28	579	49.2	204	2	06T4U1
29	579	49.2	225	2	AA87685
30	579	49.2	225	2	091LA1
31	576	48.9	210	2	AA846017
					Q710H8

32	576	48.9	210	2	CA012071	Cad12071 asarum ca
33	574	48.8	204	2	06T4U2	06T4U2 drims wint
34	574	48.8	204	2	AA87684	AA87684 drims w1
35	573.5	48.7	238	2	084U28	084U28 populus tom
36	570.5	48.5	240	2	06UVI1	06UVI1 populus tom
37	570.5	48.5	240	2	AA083493	AA83493 populus t
38	570	48.4	200	2	06T4U0	06T4U0 drims wint
39	570	48.4	200	2	AA87686	AA87686 drims w1
40	567.5	48.2	201	2	06T4V0	06T4V0 saruma hent
41	567.5	48.2	201	2	AA87676	AA87676 saruma he
42	565	48.0	226	2	09ZS28	09ZS28 gerdera hyb
43	562	47.7	200	2	06T4S9	06T4S9 lindera ery
44	562	47.7	200	2	AA87697	AA87697 lindera e
45	558	47.4	200	2	06T4U3	06T4U3 drims wint

ALIGNMENTS

RESULT 1	ID	084M23	PRELIMINARY;	PRT;	225 AA.
AC	084M23;				
DT	01-JUN-2003 (TrEMBLrel. 24, Created)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	MADS-box transcription factor.				
GN	Name=AODEF;				
OS	Asparagus officinalis (Garden asparagus).				
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Asparagaceae;				
OC	Asparagus.				
OX	NCBI_TaxID=4686;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Flower;				
RA	Park J., Ishikawa Y., Yoshida R., Kanno A., Kameya T.;				
RT	"Expression of AODEF, a B-functional MADS-box gene, in stamens and				
RL	inner tepals of dioecious species Asparagus officinalis L.";				
CC	-1- SUBCELLULAR LOCATION: Nuclear (By similarity).				
CC	-1- SIMILARITY: Contains 1 MADS-box domain.				
DR	EMBL; AB094964; BAC75569.1; -.				
DR	HSSP; P11746; IMNM.				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003700; F:transcription factor activity; IEA.				
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR	InterPro; IPR002487; TF_Rbox.				
DR	InterPro; IPR002100; TF_MADSbox.				
DR	Pfam; PF01486; K-box; 1.				
DR	Pfam; PF00319; SRP-TF; 1.				
DR	PRINTS; PR00404; MADSDOMAIN.				
DR	SMART; SM00432; MADS; 1.				
DR	PROSITE; PS00350; MADS_BOX_1; 1.				
DR	PROSITE; PS50066; MADS_BOX_2; 1.				
KW	DNA-binding; Nuclear protein; Transcription regulation.				
SQ	SEQUENCE 225 AA; 25774 MW; 8E946D2848B2EDCF CRC64;				
Query Match	69.7%;	Score 820;	DB 2;	Length 225;	
Best Local Similarity	68.7%;	Pred. No. 4,7e-51;			
Matches 156;	Conservative 37;	Mismatches 32;	Indels 2;	Gaps 2;	
QY	1	MGRGKIEIKIENPTNRQVYTSKRRVGLKAKELTVLCDAQVSLIMFSSTGLADYCS	60		
DB	1	MGRGKIEIKIENPTNRQVYTSKRRVGLKAKELTVLCDAQVSLIMFSSTGLADYCS	60		
QY	61	STDIKIERRYQVYVGMGLMNAQYERMONTLGHININONLKEIKERRRGEELGMDIQ	120		
DB	61	GSOTKAIIPRYOQAVGINLMSAQYEMONTLGHLEIKINNLKRELIRQRTGEELGMDIE	120		
QY	121	LRLQEQTLSESLRIYHRKRYHVIATQDTYKKKLKSTREYALIHLELMKEENPNYGFN	180		
DB	121	LRLQEQNLDEALIKLVYHRKRYHVIISTQDTYKKKLKSTREYALIHLELMKEENPNYGFN	180		

QY 181 VENOSRIYENSIPWNECPQMSFRVYVHPNPNILGLGYESHDLISLA 227
 DB 181 DEDSN-YEGALALANGSHVAFR-VQPSQPNLHGMGCGPHDLRLA 225

RESULT 2

Q8LTL10 ID Q8LTL10 PRELIMINARY; PRT; 228 AA.
 AC Q8LTL10;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE MADS-box transcription factor.
 GN Name=MADS1;
 OS Liliaceae (Regal Lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxId=82328;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=21959322; PubMed=11961093;
 RA Winter K.U., Weiser C., Kaufmann K., Bohne A., Kirchner C., Kanno A.,
 SA Siedler H., Theissen G.,
 RT "Evolution of class B floral homeotic proteins: obligate
 heterodimerization originated from homodimerization.",
 RL Mol. Biol. Evol. 19:587-596(2002).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AB071378; BAB91550.1; -.
 DR HSSP; P11746; 1MNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 DR DNASIS; PS0066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 228 AA; 26193 MW; 760321C381A06A5B CRC64;

Query Match Best Local Similarity 66.5%; Score 782.5; DB 2; Length 228;
 Matches 149; Conservative 42; Mismatches 34; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYSKRVRGILKKAKELTVLDCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYSKRVRGILKKAKELTVLDCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYOVTGMDLMAQYERQNTLKLINQNLKRIKRRKGEELGMDIKQ 120
 DB 61 STDIKGIYERYOVTGMDLMAQYERQNTLKLINQNLKRIKRRKGEELGMDIKQ 120
 QY 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 DB 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 QY 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 DB 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 QY 178 GFVVENQSRITYENSIPWNECPQMSFRVYVHPNPNILGLGYESHDLISLA 227
 DB 178 GFVVENQSRITYENSIPWNECPQMSFRVYVHPNPNILGLGYESHDLISLA 227
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, last sequence update)

DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE MADS box protein.
 GN Name=MADS1;
 OS Lilium longiflorum (Trumpet Lily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Lilium.
 OX NCBI_TaxId=4690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21510302; PubMed=11673632;
 RA Tzeng T.-Y., Yang C.-H.;
 RT "A MADS box gene from Lily (Lilium longiflorum) is sufficient to
 generate dominant negative mutation by interacting with PISTILLATA
 (PI) in Arabidopsis thaliana.",
 RL Plant Cell Physiol. 42:1156-1168(2001).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AF503913; AAM27456.1; -.
 DR HSSP; P11746; 1MNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS0066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 228 AA; 26179 MW; 7606B9C21A06A5B CRC64;

Query Match Best Local Similarity 66.4%; Score 781.5; DB 2; Length 228;
 Matches 149; Conservative 42; Mismatches 34; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYSKRVRGILKKAKELTVLDCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKIENPTNRQVYSKRVRGILKKAKELTVLDCDAQVSLMFSTGKLADYCSF 60
 QY 61 STDIKGIYERYOVTGMDLMAQYERQNTLKLINQNLKRIKRRKGEELGMDIKQ 120
 DB 61 STDIKGIYERYOVTGMDLMAQYERQNTLKLINQNLKRIKRRKGEELGMDIKQ 120
 QY 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 DB 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 QY 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 DB 121 LRGLGQLTLESRLIVRRKRVHVAATQDTYKKKLSSTRETYALHLEL--DKKENPNY 177
 QY 178 GFVVENQSRITYENSIPWNECPQMSFRVYVHPNPNILGLGYESHDLISLA 227
 DB 178 GFVVENQSRITYENSIPWNECPQMSFRVYVHPNPNILGLGYESHDLISLA 227
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE Putative MADS box transcription factor.
 GN Name=MADS1;
 OS Hemerocallis sp. (Daylily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 OC Hemerocallidaceae; Hemerocallis.
 OX NCBI_TaxId=29711;
 RN [1]

RESULT 4

Q9FR12 ID Q9FR12 PRELIMINARY; PRT; 221 AA.
 AC Q9FR12;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
 DE Putative MADS box transcription factor.
 GN Name=MADS1;
 OS Hemerocallis sp. (Daylily).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
 OC Hemerocallidaceae; Hemerocallis.
 OX NCBI_TaxId=29711;
 RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Petal;
RA Lange N.E.;
RT "Molecular changes during the expansion and senescence of ethylene-
RT insensitive daylily flowers.";
RT Thesis (1999). University of California, Davis.
RL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AF209729; AAC35773.1; -.
DR HSSP; Q02078; IEGW.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 221 AA; 25357 MW; AB5DC7E3D7FDB4B8 CRC64;

Query Match 62.7%; Score 738; DB 2; Length 221;
Best Local Similarity 63.4%; Pred. No. 3,5e-45;
Matches 144; Conservative 35; Mismatches 42; Indels 6; Gaps 3;

QY 1 MGRGKIEIKKIEPTNRQVTSKRRVGLTKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNRQVTSKRRVGLTKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
QY 61 STDIKGIERYRYQVVTGMDLMAQYERMQNTLKLINLNONLRKEIRRKGEELGMDIKQ 120
DB 61 STDIKGIERYRYQVVTGMDLMAQYERMQNTLKLINLNONLRKEIRRKGEELGMDIKQ 120
QY 61 GTDTKTVFERYQATQNTLMSTQYKKQNTLNHLKEINHLRKEIRRGIGELDGMDFKE 120
DB 61 GTDTKTVFERYQATQNTLMSTQYKKQNTLNHLKEINHLRKEIRRGIGELDGMDFKE 120
QY 121 LRGLGQTLSESLIYVRRKRVHATQTDYKKLKSRETRYRALIHL--DKKEENPNY 180
DB 121 LRGLGQTLSESLIYVRRKRVHATQTDYKKLKSRETRYRALIHL--DKKEENPNY 180
QY 121 LRLEQNLLEBALXIVARKYHVTITQDTYKKVKSQEHAKTLHL--DAVGYA 176
DB 121 LRLEQNLLEBALXIVARKYHVTITQDTYKKVKSQEHAKTLHL--DAVGYA 176
QY 181 VENQSRIRYENSIPMNECPQSFRRVHPNPQNLGLGYSHLSLA 227
DB 177 DEDPGN-YDSSLALHAGSSNMYR-VQSPQNLHGWSYPPHRLA 221

RESULT 5
Q84M22 PRELIMINARY; PRT; 228 AA.
AC 084M22;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MADS-box transcription factor.
GN Name=TCDBFA.
OS Tulipa gesneriana (Tulip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
ON NCBI_TaxID=13306;
RX TISSUE=Flower;
RC MEDLINE=22856392; PubMed=13677470;
RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;
RT "Heterotopic expression of class B floral homeotic genes supports a
RT modified ABC model for tulip (Tulipa gesneriana).";
RL Plant Mol. Biol. 52:831-841(2003).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AB094965; BAC75970.1; -.
DR HSSP; P11746; IMNM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

```

```

DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 228 AA; 26379 MW; P9D47499317A2F98 CRC64;

Query Match 62.1%; Score 730.5; DB 2; Length 228;
Best Local Similarity 61.3%; Pred. No. 1,3e-44;
Matches 141; Conservative 44; Mismatches 40; Indels 5; Gaps 3;

QY 1 MGRGKIEIKKIEPTNRQVTSKRRVGLTKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNRQVTSKRRVGLTKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
QY 61 STDIKGIERYRYQVVTGMDLMAQYERMQNTLKLINLNONLRKEIRRKGEELGMDIKQ 120
DB 61 STDIKGIERYRYQVVTGMDLMAQYERMQNTLKLINLNONLRKEIRRKGEELGMDIKQ 120
QY 61 STQKKIFRYQQTGIMNSAQYERMQNTFNLQINRLRREIKQRMGEELDGLDFSE 120
DB 61 STQKKIFRYQQTGIMNSAQYERMQNTFNLQINRLRREIKQRMGEELDGLDFSE 120
QY 121 LRGLGQTLSESLIYVRRKRVHATQTDYKKLKSRETRYRALIHL--DKKEENPNY 177
DB 121 LRGLGQTLSESLIYVRRKRVHATQTDYKKLKSRETRYRALIHL--DKKEENPNY 177
QY 178 GFVENQSRIRYENSIPMNECPQSFRRVHPNPQNLGLGYSHLSLA 227
DB 181 GY-IDDDPNSEGGGLALANGSSMYER-VQSPQNLHGWSYPPHRLA 228

RESULT 6
Q84UA4 PRELIMINARY; PRT; 204 AA.
AC 084UA4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MADS box protein.
GN Name=MADS3.
OS Oncidium cv. 'Gower Ramsey'.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
OC Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;
OC Oncidium.
ON NCBI_TaxID=96474;
RX TISSUE=Flower;
RC MEDLINE=22294943; PubMed=12407200;
RA Heu H.-F., Yang C.-H.;
RT "An orchid (Oncidium Gower Ramsey) AP3-like MADS gene regulates floral
RT formation and initiation.";
RL Plant Cell Physiol. 43:1198-1209(2002).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 MADS-box domain.
DR EMBL; AY196350; AAC45824.1; -.
DR HSSP; P11746; IMNM.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.

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KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 204 AA; 23731 MW; 387E7C206F3CEB08 CRC64;

Query Match
 Best Local Similarity 60.8%; Score 716; DB 2; Length 204;
 Matches 139; Conservative 33; Mismatches 29; Indels 8; Gaps 2;

QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAGVSLIMFSSGTGLADYCP 60
 DB 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAGVSLIMFSSGTGLADYCP 60
 QY 61 STDIGIYERYOVYVGMGLMAQYERMTNKLHNEINONLKEIRRKGEELGMDIQ 120
 DB 61 STEIKDAFORYQOVTFDIDWDAQYRQSTLNLNLEVNKLOMETRQRKGNTLGLDYKE 120
 QY 121 LRGLQTLRESLRIVHRKHYVIAOTDTYKKKLSRETRYRALIHEL--DKKEPNYVGF 179
 DB 121 LRGLQTLRESLRIVHRKHYVIAOTDTYKKKLSRETRYRALIHEL--DKKEPNYVGF 179
 QY 180 NVENOSRIYENSIPMNECPQMFSPRVVH 208
 DB 181 IAEIDLGVNYSALISMANQ-----RLAH 202

RESULT 7

ID Q84M21 PRELIMINARY; PRT; 231 AA.
 AC Q84M21;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE MADS-box transcription factor.
 GN Name=TDDBF;
 OS Tulipa gesneriana (Tulip).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae; Tulipa.
 OX NCBI_TaxID=3306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=22856392; PubMed=13677470;
 RA Kanno A., Saeki H., Kameya T., Saedler H., Theissen G.;
 RT "Heteroctic expression of class B floral homeotic genes supports a
 RL modified ABC model for tulip (Tulipa gesneriana).";
 CC Plant Mol. Biol. 52:831-841(2003).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AB094966; BAC75971.1; -.
 DR HSSP; P11746; IMNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1_MADSbox.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 231 AA; 26568 MW; 8CA6830BE83800C0 CRC64;

Query Match
 Best Local Similarity 59.6%; Score 701.5; DB 2; Length 231;
 Matches 136; Conservative 45; Mismatches 44; Indels 5; Gaps 3;

QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAGVSLIMFSSGTGLADYCP 60
 DB 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAGVSLIMFSSGTGLADYCP 60
 QY 61 STDIGIYERYOVYVGMGLMAQYERMTNKLHNEINONLKEIRRKGEELGMDIQ 120
 DB 61 STDIGIYERYOVYVGMGLMAQYERMTNKLHNEINONLKEIRRKGEELGMDIQ 120

DB 61 STNCKIFRYYQMTGINLMSAQYERMTNHLSQLNRRLREIKQRMGEQLDGLDSNE 120

QY 121 LRGLQTLRESLRIVHRKHYVIAOTDTYKKKLSRETRYRALIHEL--DKKEPNY 177
 DB 121 LRGLQTLRESLRIVHRKHYVIAOTDTYKKKLSRETRYRALIHEL--DKKEPNY 177
 QY 178 GFVNENOSRIYENSIPMNECPQMFSPRVVHNPQNLGLGYSHDLSTA 227
 DB 181 GY-VDDPNYSYEGGIALANGSSMYEER-IQSPQNLHGNGYGLHDLCLS 228

RESULT 8

ID Q9LL99 PRELIMINARY; PRT; 200 AA.
 AC Q9LL99;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DE 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE MADS box transcription factor AP3 (Fragment).
 OS Tacca chantleri (Bat flower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Taccac.
 OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;
 OX NCBI_TaxID=85283;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kramer E.M., Irish V.F.;
 RA "Evolution of the petal and stamen developmental programs: Evidence
 RT from comparative studies of the lower eudicots and basal
 RL angiosperms."; Int. J. Plant Sci. 0:0-0(2000).
 CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -|- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF230706; AAF73935.1; -.
 DR HSSP; 002078; IBCW.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1_MADSbox.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 200 AA; 23218 MW; 930A6804757C464C CRC64;

Query Match
 Best Local Similarity 59.5%; Score 700; DB 2; Length 200;
 Matches 130; Conservative 39; Mismatches 30; Indels 2; Gaps 2;

QY 27 GILKKAKELTVLCDAGVSLIMFSSGTGLADYCPSTDIKGIYERYOVYVGMGLMAQYER 86
 DB 2 GILKKAKELTVLCDAGVSLIMFSSGTGLADYCPSTDIKGIYERYOVYVGMGLMAQYER 86
 QY 87 MONTLKLHNEINONLKEIRRKGEELGMDIQDLQGLQTLRESLRIVHRKHYVIAOT 146
 DB 87 MONTLKLHNEINONLKEIRRKGEELGMDIQDLQGLQTLRESLRIVHRKHYVIAOT 146
 QY 147 TDYTKKLSKRETRYRALIHELDMKEENPNYGVNENOSRIYENSIPMNECPQMFSPRV 206
 DB 122 TDYTKKLSKRETRYRALIHELDMKEENPNYGVNENOSRIYENSIPMNECPQMFSPRV 206
 QY 207 VHPNPNLGLGYSHDLSTA 227
 DB 180 VQSPQNLHGNGYGLHDLSTA 227

RESULT 9

ID Q9XJ65 PRELIMINARY; PRT; 224 AA.
 AC Q9XJ65;

DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MADS-box-like protein.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarthroideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RX NCBI_TaxID=39947;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Panicle at meiotic stage;
 RA Shinozuka Y., Yamamoto K., Sasaki T.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AB003323; BAA1881.1; -.
 DR HSSP; P11746; 1MNM.
 DR Gramene; O94459; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 224 AA; 25464 MW; A8739E83F936A8E6 CRC64;
 SQ

Query Match 58.2%; Score 684.5; DB 2; Length 224;
 Best local similarity 60.4%; Pred. No. 2.5e-41;
 Matches 138; Conservative 34; Mismatches 50; Indels 5; Gaps 5;

QY 1 MGRGKIEIKIENPTROVYTSKRRVGLKKAKELTVLCDAQVSLMFSGTKLADYCSF 60
 DB 1 MGRGKIEIKIENATROVYTSKRRVGLKKAKELTVLCDAQVSLMFSGTKLADYCSF 60
 QY 61 STDIKGIIFRYQQAIGTSLMIEYEMQRTLSHKDINRLRIRKQMGEDLDGLEFDE 120
 DB 61 STDIKGIIFRYQQAIGTSLMIEYEMQRTLSHKDINRLRIRKQMGEDLDGLEFDE 120
 QY 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 QY 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 QY 181 VENQSRIVYENSIPWNECPMFSEFRVHPNPQNLGLGY-ESHDLSL 226
 DB 181 VENQSRIVYENSIPWNECPMFSEFRVHPNPQNLGLGY-ESHDLSL 226
 DB 179 VDNVTGGWDGAG-AGAAADMFAFRVY-PSQPNLHGMAVGNHDLRL 223

RESULT 10
 Q94459 PRELIMINARY; PRT; 224 AA.
 AC Q94459;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MADS-box protein SPW1.
 GN Name=SPW1;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriarthroideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RX NCBI_TaxID=39947;
 RN
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22392989; PubMed=12506001;
 RA Nagasawa N., Miyoshi M., Sano Y., Satoh H., Hirano H., Sakai H.,
 RA Nagata Y.;
 RT "SUPERMOMANI and DROOPING LEAF genes control floral organ identity in

RT rice";
 RL Development 130:705-718(2003).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF424549; AAL18851.1; -.
 DR HSSP; P11746; 1MNM.
 DR Gramene; O94459; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 224 AA; 25463 MW; 48953A43D2E270 CRC64;
 SQ

Query Match 57.8%; Score 680.5; DB 2; Length 224;
 Best local similarity 60.4%; Pred. No. 4.8e-41;
 Matches 137; Conservative 35; Mismatches 50; Indels 5; Gaps 5;

QY 1 MGRGKIEIKIENPTROVYTSKRRVGLKKAKELTVLCDAQVSLMFSGTKLADYCSF 60
 DB 1 MGRGKIEIKIKATROVYTSKRRVGLKKAKELTVLCDAQVSLMFSGTKLADYCSF 60
 QY 61 STDIKGIIFRYQQAIGTSLMIEYEMQRTLSHKDINRLRIRKQMGEDLDGLEFDE 120
 DB 61 STDIKGIIFRYQQAIGTSLMIEYEMQRTLSHKDINRLRIRKQMGEDLDGLEFDE 120
 QY 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 QY 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 DB 121 LRGLQTLBESLRIVRRKXVIAATQTDYKKLKRSTETRYALIHLDKKEENPNYGFN 180
 QY 181 VENQSRIVYENSIPWNECPMFSEFRVHPNPQNLGLGY-ESHDLSL 226
 DB 181 VENQSRIVYENSIPWNECPMFSEFRVHPNPQNLGLGY-ESHDLSL 226
 DB 179 VDNVTGGWDGAG-AGAAADMFAFRVY-PSQPNLHGMAVGNHDLRL 223

RESULT 11
 Q9M6N9 PRELIMINARY; PRT; 227 AA.
 AC Q9M6N9;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MADS-box DNA binding protein.
 GN Name=silky1;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; panicoidae; Andropogoneae; Zea.
 NCBI_TaxID=4577;
 RX NCBI_TaxID=4577;
 RN
 RP SEQUENCE FROM N.A.
 RA Ambrose B.A., Lerner D.R., Ciceri P., Padilla C., Yanofsky M.,
 RA Schmidt R.J.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF181479; AAF59838.1; -.
 DR HSSP; P11746; 1MNM.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSOMAIN.
 DR SMART; SM00432; MADS; 1.

DR PROSITE: PS50066; MADS_BOX.2; 1.
 KW DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 227 AA; 25841 MW; 22AC1DAAB51742E1 CRC64;

Query Match 57.3%; Score 675; DB 2; Length 227;
 Best Local Similarity 59.0%; Pred. No. 1,2e-40;
 Matches 135; Conservative 37; Mismatches 51; Indels 6; Gaps 5;

QY 1 MGRGKIEIKIENPTNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVYTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKHLEINONLRKEIRRKKEELEGMIDIQ 120
 DB 61 GTDIKTIIPDRYQQAIGTSLMIEQYENMORTLSHLKDINRLRTEIRIQRMGEIDLGLDFDE 120
 QY 121 LRGLQTLLESRLIVRRKRYHIVATQTDYTKKKLSTRETYRALIHELDKKEENPYNGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHIVSTQDTYKKYKSHYKXVKTLOGLGMRD-PAYGF- 178
 QY 181 VENOSR--IYENSIPVNEC-PQWFSFRVYHPNPMLIGLYESHDL 226
 DB 179 VDNAGAGVAMDGAALGAPPMYAFRV-PSQPNLHGMAVGFHDLRL 226

RESULT 12

Q9ZPM9 PRELIMINARY; PRT; 223 AA.

DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MADS box protein.
 GN Name=MADS16;
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99320878; PubMed=10394955;
 RA Moon Y.-H., Jung J.-Y., Kang H.-G., An G.;
 RT "Identification of a rice APTALA3 homologue by yeast two-hybrid
 screening.";
 RL Plant Mol. Biol. 40:167-177 (1999).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Moon Y.-H., Jung J.-Y., An G.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AF077760; AAD19872.1; -;
 DR HSSP; P11746; 1MM.
 DR TRANSPAC; T05232; -;
 DR Gtrameae; Q9ZPM9; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription; IEA.
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS.1.
 DR PROSITE; PS50066; MADS_BOX.2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 223 AA; 25377 MW; F3CA59798640EDC4 CRC64;

Query Match 56.4%; Score 664; DB 2; Length 223;
 Best Local Similarity 59.0%; Pred. No. 7,3e-40;
 Matches 134; Conservative 36; Mismatches 51; Indels 6; Gaps 4;

QY 1 MGRGKIEIKIENPTNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVYTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKHLEINONLRKEIRRKKEELEGMIDIQ 120
 DB 61 GTDIKTIIPDRYQQAIGTSLMIEQYENMORTLSHLKDINRLRTEIRIQRMGEIDLGLDFDE 120
 QY 121 LRGLQTLLESRLIVRRKRYHIVATQTDYTKKKLSTRETYRALIHELDKKEENPYNGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHIVSTQDTYKKYKSHYKXVKTLOGLGMRD-PAYGF- 177
 QY 181 VENOSRIYENSIPVNEC-PQWFSFRVYHPNPMLIGLY-ESHDL 226
 DB 178 VDNAGAGVAMDGAAGAAADMFARV-PSQPNLHGMAVGFHDLRL 222

RESULT 13

Q6OH13

ID Q6OH13 PRELIMINARY; PRT; 232 AA.

AC Q6OH13;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE APTALA3-like protein.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticaceae; Hordeum.
 OX NCBI_TaxID=112509;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Allen R.L., Turner A., Laurie D.A.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL; AY541065; AAS48126.1; -;
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF01486; K-box; 1.
 DR Pfam; PF00319; SRF-TF; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS.1.
 DR PROSITE; PS50066; MADS_BOX.2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 KW SEQUENCE 232 AA; 26333 MW; 13DCC437D57F4C94 CRC64;

Query Match 56.3%; Score 663; DB 2; Length 232;
 Best Local Similarity 59.0%; Pred. No. 9e-40;
 Matches 135; Conservative 37; Mismatches 49; Indels 8; Gaps 5;

QY 1 MGRGKIEIKIENPTNRQVYTSKRRVGLIKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 DB 1 MGRGKIEIKRIENATNRQVYTSKRRGTIMKKARELTVLCDAQVALIMFSSGTGKHEFCSP 60
 QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKHLEINONLRKEIRRKKEELEGMIDIQ 120
 DB 61 GTDIKTIIPDRYQQAIGTSLMIEQYENMORTLSHLKDINRLRTEIRIQRMGEIDLGLDFDE 120
 QY 121 LRGLQTLLESRLIVRRKRYHIVATQTDYTKKKLSTRETYRALIHELDKKEENPYNGFN 180
 DB 121 LRGLQNVDAALKEVRKRYHIVSTQDTYKKYKSHYKXVKTLOGLGMRD-PAYGF- 178
 QY 181 VENOSRIYENSIPVNEC-PQWFSFRVYHPNPMLIGLY-ESHDL 224
 DB 179 VDNPAAGWDGVAALVAMGGSAADMYAFRV-PSQPNLHGMAVGGSHDL 226

RESULT 14

AAS48126 PRELIMINARY; PRT; 232 AA.
 ID AAS48126;
 AC AAS48126;
 DT 10-MAR-2004 (TrEMBLrel. 27, Created)

DT 10-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 10-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE APEXLAJ-like protein.
 OS Hordeum vulgare var. distichum (Two-rowed barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum; Hordeum vulgare.
 NC NCB1_TaxID=112509;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Forester;
 RA Allen R.L., Turner A., Laurie D.A.;
 RT "MADS-box transcription factors of barley";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY541065; AAS48126.1; -
 SQ SEQUENCE 232 AA; 26333 MW; 13DC437D57F4C94 CRC64;
 Query Match 56.3%; Score 663; DB 2; Length 232;
 Best Local Similarity 59.0%; Pred. No. 9e-40; Indels 8; Gaps 5;
 Matches 135; Conservative 37; Mismatches 49;
 QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIENATNRQVTSKRRSGIMKKAKELTVLCDAQVAIIFFSTGKHYECST 60
 QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINQLRKEIRRRKGEELGMDIKQ 120
 DB 61 GTDIKGIIPRYQQAIGTSLMIEQYENMORTLSHKDINRLKTEIRRMEDDLDALEFEE 120
 QY 121 LRLEQTLBSLRLVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRLEQNVDAALKEVQRKRYHVTOTETYYKKVKHSQEAAYKNLQOELGWRD-PAYGF- 178
 QY 181 VENQSRITYENSIPMV---NECPQMFSEFRVYHNPQNLGLG-ESHDL 224
 DB 179 VDNPAAGMGDVAVAVMGGGSAADMYAFRV-PSQPNLHGMAVGSHDL 226
 RESULT 15
 082130 PRELIMINARY; PRT; 229 AA.
 ID 082130;
 AC 082130;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MADS box transcription factor.
 GN Name=TAMADS#51;
 OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 NC NCB1_TaxID=4565;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young spike;
 RA Mural K., Mural R., Takumi S., Ogihara Y.;
 RT "cDNA cloning of three MADS box genes in wheat (Accession Nos.
 RL AB007504, AB007505 and AB007506) (PGR98-159).";
 RL Plant Physiol. 118:330-330(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young spike;
 RX MEDLINE=21841579; PubMed=11851918;
 RA Mural K., Takumi S., Koga H., Ogihara Y.;
 RT "Pistillody, homeotic transformation of stamens into pistil-like
 RT structures, causes by nuclear-cytoplasm interaction in wheat.";
 RL Plant J. 29:165-181(2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Young spike;
 RA Mural K., Mural R., Takumi S., Ogihara Y.;
 RT "Cloning and characterization of cDNAs corresponding to the wheat MADS
 RT box genes.";

RL (in) Slinkard A.E. (eds.);
 RL Proceedings of the 9th International wheat Genetics Symposium.
 RL pp.89-94, University Extension Press, Saskatoon, Canada (1998).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: Contains 1 MADS-box domain.
 DR EMBL: AB007506; BAA33459.1; -
 DR HSP: P11746; 1NM.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SR-TF; 1.
 DR PRINTS: PR00404; MADSBOXMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DNA-binding; Nuclear protein; Transcription regulation.
 SQ SEQUENCE 229 AA; 26038 MW; 1CF57CBA6AA3157 CRC64;
 Query Match 55.5%; Score 653; DB 2; Length 229;
 Best Local Similarity 58.4%; Pred. No. 4.6e-39;
 Matches 135; Conservative 36; Mismatches 52; Indels 8; Gaps 5;
 QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLMFSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIENATNRQVTSKRRSGIMKKAKELTVLCDAQVAIIFFSTGKHYECST 60
 QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINQLRKEIRRRKGEELGMDIKQ 120
 DB 61 GTDIKGIIPRYQQAIGTSLMIEQYENMORTLSHKDINRLKTEIRRMEDDLDALEFEE 120
 QY 121 LRLEQTLBSLRLVHRKRYVATOTDTYKKKLSKSTRETYRALIHELDKKEENPNYGFN 180
 DB 121 LRLEQNVDAALKEVQRKRYHVTOTETYYKKVKHSQEAAYKNLQOELGWRD-PAYGF- 178
 QY 181 VENQSRITYENSIPMV---NECPQMFSEFRVYHNPQNLGLG-ESHDL 226
 DB 179 VDNPAAGMGDVAVAVMGGGLAADMYAFRV-PSQPNLHGMAVGSHDL 228
 Search completed: January 27, 2005, 13:21:27
 Job time : 196 secs

TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-10

Query Match
Best Local Similarity 29.0%; Score 341.5; DB 2; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKKINPTNRQVYSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGVELEKRIENKINRQVTSKRTGLKKAKQISVLCDAEVSILVFSHGKLFYSS 60
QY 61 SDIDGI--YERYQV-----VTGMDLNAQYERMONTLKHINEINOMLRKEIRR 107
DB 61 SCMEVLEKRIERYRYAERQLIAPDSHVNAQTNWMEYSRLKAKIE-LLENNQ-----RH 113
QY 108 RKGELSEMDIKOLRGLEQTLSESLRIVRRKHYVIAOTDTYKKKLSKSTREYRALIHE 167
DB 114 YLGELEPMSLKDQNLQEQLETALKHIRSRKQQLMNEISLNHLQREKEKEIQEENSMLTQ 173
QY 168 LDMKEENPNYGFVNENSRIVENSIPVWNECPOMFS---FRVWHNPQ--NLLGIGYES 221
DB 174 I--KERENILIKTKQTCQELNRSVDVDPQ-PQPFQPHLYMIAHOTSPFLNMGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 3
US-08-659-188-10
Sequence 10, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofeky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California

COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-10

Query Match
Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKKINPTNRQVYSKRRVGLKKAKELTVLCDAQVSLIMFSSGKLADYCSF 60
DB 1 MGRGVELEKRIENKINRQVTSKRTGLKKAKQISVLCDAEVSILVFSHGKLFYSS 60
QY 61 SDIDGI--YERYQV-----VTGMDLNAQYERMONTLKHINEINOMLRKEIRR 107
DB 61 SCMEVLEKRIERYRYAERQLIAPDSHVNAQTNWMEYSRLKAKIE-LLENNQ-----RH 113
QY 108 RKGELSEMDIKOLRGLEQTLSESLRIVRRKHYVIAOTDTYKKKLSKSTREYRALIHE 167
DB 114 YLGELEPMSLKDQNLQEQLETALKHIRSRKQQLMNEISLNHLQREKEKEIQEENSMLTQ 173
QY 168 LDMKEENPNYGFVNENSRIVENSIPVWNECPOMFS---FRVWHNPQ--NLLGIGYES 221
DB 174 I--KERENILIKTKQTCQELNRSVDVDPQ-PQPFQPHLYMIAHOTSPFLNMGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 4
US-08-655-227-10
Sequence 10, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofeky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APTETAL1 Gene
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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1 APPLICATION NUMBER: US/08/655,227
2 FILING DATE: 05-JUN-1996
3 CLASSIFICATION: 800
4
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Campbell, Cathryn A.
7 REGISTRATION NUMBER: 31,815
8 REFERENCE/DOCKET NUMBER: P-UD 2143
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (619) 535-9001
11 TELEFAX: (619) 535-8949
12 INFORMATION FOR SEQ ID NO: 10:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 255 amino acids
15 TYPE: amino acid
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 US-08-655-227-10
19
20 Query Match 29.0%; Score 341.5; DB 3; Length 255;
21 Best Local Similarity 37.6%; Pred. No. 7.4e-26;
22 Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9
23
24 QY 1 MGRGKIEIKTIENPTNRQVTSKRRVGIKKAKELTVLDAQVSLIMFSSTGLADYCSF 60
25 1 MGRGVELKRIENKINRQVTFSEKRTGILKKRQGLSVLCDAVSLVFHKKKLPYSS 60
26
27 QY 61 STDIKGI--YERYQV-----VTGMDLMAQYERMONTLKLHINONLRKEIR 107
28 61 SCMEVFLRYERYRYSAEROLIPDSDHVAQAQTWMSMEYSRLKAKIE--ILERNQ-----RH 113
29
30 QY 108 RKGELEBMDIKQALGRLBQTLSESLRIVHRKYNHVIATQTDVYKKKLSRETYRALNH 167
31 114 YLGEELBPMSLDLDLNLQQLSTALKHTRSRXNQLNBSLNHLQREKEXIOBNSNLTQY 173
32
33 QY 168 LDMKEENNYGFNVNQSRIVENSIPMYNECPOMFS---FVYVHPNCP--NLLGLGYES 221
34 Db 174 I--KERENILKTQYQCEQLNRSYDVPDQ--PQRFQPHLVMLAQTSTFLMAGL--YQG 228
35
36 QY 222 HD 223
37 Db 229 ED 230
38
39 RESULT 5
40 US-08-655-241-10
41 Sequence 10, Application US/08655241
42 Patent No. 6025543
43 GENERAL INFORMATION:
44 APPLICANT: Yanofsky, Martin F.
45 APPLICANT: Weigelt, Detlef
46 TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
47 TITLE OF INVENTION: Development and Methods of Making Same
48 NUMBER OF SEQUENCES: 26
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: Campbell and Flores
51 STREET: 4370 La Jolla Village Drive, Suite 700
52 CITY: San Diego
53 STATE: California
54 COUNTRY: USA
55 ZIP: 92122
56
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: Patent Release #1.0, Version #1.25
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/08/655,241
64 FILING DATE: 05-JUN-1996
65 CLASSIFICATION: CLASS 800
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Campbell, Cathryn A.
68 REGISTRATION NUMBER: 31,815
69 REFERENCE/DOCKET NUMBER: P-UD 1894

```

```

; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 255 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
; US-08-655-241-10

Query Match      29.0%; Score 341.5; DB 3; Length 255;
Best Local Similarity 37.6%; Pred. No. 7.4e-26;
Matches    91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY      1 MGKGIETIKIENPTNQVTSKRVRGILKKAKELTVLCDAQVSLMFSSTGLADYCSP 60
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1 MGRGVLEIKRIENKINRQWTFPSKRTGLTKKAORISVLCDABEASLIVFSHKGKLFEYSSE 60
         |-----YTGDMLNNAQVERNQTJKNLENNONRKREIR 107
QY      61 STDJKGT--VRRYQV-----                                113
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      61 SCMEKVLRERYRYAYARQLAPDSHVAOQTWSMEYSRLAKTE-LIERNQ-----RH 113
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      108 RKGEELSGMDIKDPRGLEQTLESRLIVRRHKYVIATOTDTYKKLKLSRETFRALIIHE 167
          ||||::||||::||||::||||::||||::||||::||||::||||::||||
DB      114 YLGSELPEMSIAKDIONIEQQLETALKAIRSKRNQNMBSLNHLDRKEKEIOENSMTLKQ 173
          ||||::||||::||||::||||::||||::||||::||||::||||::||||
QY      168 LDMKENPNNGFNVENOSRIYENSIPMNVECPWFSS---FRVVHPNP--NLIGLYES 221
          ||||::||||::||||::||||::||||::||||::||||::||||::||||
DB      174 I---KERENILKTQTCCQLNRGSVDVPQ-PQPFGPHPLYMIHQPSPLFMWGGL-YQG 228
          ||||::||||::||||::||||::||||::||||::||||::||||::||||
QY      222 HD 223
         |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      229 ED 230
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 6
US-09-149-976-10
; Sequence 10, Application US/09149976
; Patent No. 6127123
; GENERAL INFORMATION:
;   APPLICANT: Yanofsky, Martin F.
;   TITLE OF INVENTION: Cauliflower Floral Meristem Identity
;   TITLE OF INVENTION: Genes and Methods of Using Same
;   NUMBER OF SEQUENCES: 33
;   CORRESPONDENCE ADDRESSES:
;     ADDRESSEE: Campbell & Flores LLP
;     STREET: 4370 La Jolla Village Drive, Suite 700
;     CITY: San Diego
;     STATE: California
;     COUNTRY: United States
;     ZIP: 92122
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/149,976
;   FILING DATE: 09-SEP-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/592,214
;   FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Campbell, Cathryn A.
;   REGISTRATION NUMBER: 31,815
;   REFERENCE/DOCKET NUMBER: P-U2 3291
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
;   INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:

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LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-149-976-10

Query Match

Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKKIENPTNRQVTYSKRVRGILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFSKRRTGLKKAQISVLCDAEVLIVFSHGKLFYSSSE 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAQYERMONTLKHLNEINONLKEIR 107
DB 61 SCMEKVLERYERYSYAERQLIAPDSHVNAQTNMSMEYSRLKAKIE-LLENNQ-----RH 113
QY 108 RKGEELEGMDIKQALRGLEQTLAESLRIVRHRKYHVIATQDTYKKLSTRETYRALIHE 167
DB 114 YLGELEPMSLKDLQNLQLEQLETLAKHRSRKNQNMESLNHLQKKEKEIQEENSMLTKQ 173
QY 168 LDMKEENPNYGFVENVQSRIVYENSIPMVNECPOMFS---FRVYHPNPQ--NLGLGYES 221
DB 174 I---KERENILKTKQTQCBQLNRSVDVPO-PQPFQHPHLWIAHQTSFPLMNGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 7

US-09-398-326-10
Sequence 10, Application US/09398326
Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Vanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-398-326-10

Query Match
Best Local Similarity 29.0%; Score 341.5; DB 3; Length 255;
Matches 91; Conservative 40; Mismatches 80; Indels 31; Gaps 9;

QY 1 MGRGKIEIKKIENPTNRQVTYSKRVRGILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFSKRRTGLKKAQISVLCDAEVLIVFSHGKLFYSSSE 60
QY 61 STDIKGI--YERYGV-----VTGMDLMAQYERMONTLKHLNEINONLKEIR 107
DB 61 SCMEKVLERYERYSYAERQLIAPDSHVNAQTNMSMEYSRLKAKIE-LLENNQ-----RH 113
QY 108 RKGEELEGMDIKQALRGLEQTLAESLRIVRHRKYHVIATQDTYKKLSTRETYRALIHE 167
DB 114 YLGELEPMSLKDLQNLQLEQLETLAKHRSRKNQNMESLNHLQKKEKEIQEENSMLTKQ 173
QY 168 LDMKEENPNYGFVENVQSRIVYENSIPMVNECPOMFS---FRVYHPNPQ--NLGLGYES 221
DB 174 I---KERENILKTKQTQCBQLNRSVDVPO-PQPFQHPHLWIAHQTSFPLMNGGL-YQG 228
QY 222 HD 223
DB 229 ED 230

RESULT 8

US-08-592-214A-12
Sequence 12, Application US/08592214A
Patent No. 5811536

GENERAL INFORMATION:

APPLICANT: Vanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
NUMBER OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-12

Query Match
Best Local Similarity 27.4%; Score 323; DB 2; Length 251;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIENPTNRQVTYSKRVRGILKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
DB 1 MGRGVEIKRIENKINRQVTFSKRRTGLKKAQISVLCDAEVLIVFSHGKLFYSSSE 60


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QY 61 STDIGI--YERYOV-----VTGMDLNAQYERONTLKLHNEINONLKEIRR 107
| : : : : :
DB 61 SCMEKLEHYERYSVAEKOLKVPDSHVNAQTNSVEYSRLKAKIE-LLEBNQ-----RH 113
| : : : : :
QY 108 RKEEELGMDIKOLRGLEOTLESRLIVRRKXHVIVATQTDYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEOQLDTSLKIRSRKQOLMHESLNHLORKEKEILEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRYEENSIPMVN 196
| : : : : :
DB 174 IRRESILRTHONOSEQONRSHHVAPQOPQLNPYMASSFFLN 216
| : : : : :

RESULT 9
US-08-659-188-12
; Sequence 12, Application US/08659188
; Patent No. 6002069
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
; TITLE OF INVENTION: Reproductive Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,188
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 1946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-188-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4.9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKLEIKKEIPTROVYTSRRVGIILKKAKELTVLCDAOYSLIMFSSTGKLADYCSF 60
| : : : : :
DB 1 MGRGRVEMKRIEIKINQVTFSSKRGAGLKKAKHEISILCDAEVSLVFSHKGLFEYSSE 60
| : : : : :
QY 61 STDIGI--YERYOV-----VTGMDLNAQYERONTLKLHNEINONLKEIRR 107
| : : : : :
DB 61 SCMEKLEHYERYSVAEKOLKVPDSHVNAQTNSVEYSRLKAKIE-LLEBNQ-----RH 113
| : : : : :
QY 108 RKEEELGMDIKOLRGLEOTLESRLIVRRKXHVIVATQTDYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEOQLDTSLKIRSRKQOLMHESLNHLORKEKEILEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRYEENSIPMVN 196
| : : : : :
DB 174 IRRESILRTHONOSEQONRSHHVAPQOPQLNPYMASSFFLN 216
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RESULT 10
US-08-655-227-12
; Sequence 12, Application US/08655227
; Patent No. 6025483
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Maize and Cauliflower APTALAI Gene
; TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655,227
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2143
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-655-227-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. No. 4.9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKLEIKKEIPTROVYTSRRVGIILKKAKELTVLCDAOYSLIMFSSTGKLADYCSF 60
| : : : : :
DB 1 MGRGRVEMKRIEIKINQVTFSSKRGAGLKKAKHEISILCDAEVSLVFSHKGLFEYSSE 60
| : : : : :
QY 61 STDIGI--YERYOV-----VTGMDLNAQYERONTLKLHNEINONLKEIRR 107
| : : : : :
DB 61 SCMEKLEHYERYSVAEKOLKVPDSHVNAQTNSVEYSRLKAKIE-LLEBNQ-----RH 113
| : : : : :
QY 108 RKEEELGMDIKOLRGLEOTLESRLIVRRKXHVIVATQTDYKKLKSRETYRALIHE 167
| : : : : :
DB 114 YLGEDDESISIKELONLEOQLDTSLKIRSRKQOLMHESLNHLORKEKEILEENSMIAKQ 173
| : : : : :
QY 168 LDMKE-----ENPNYGFNV---ENQSRYEENSIPMVN 196
| : : : : :
DB 174 IRRESILRTHONOSEQONRSHHVAPQOPQLNPYMASSFFLN 216
| : : : : :

RESULT 11
US-08-655-241-12
; Sequence 12, Application US/08655241
; Patent No. 6025543
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
; TITLE OF INVENTION: Development and Methods of Making Same
; NUMBER OF SEQUENCES: 26
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-655-241-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. NO. 4,9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIEPTNROVYTSKRVRGILKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNROVYTSKRVRGILKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIDGI--YERYQV-----VTGMDLMAQYEROMNTLKHINEINOLKREIRR 107
DB 61 SCMEKYLEHYERYVAEKQKLVPSHVAQAQTMSVEYSRLKAKTE-LLENNQ-----RH 113
QY 108 RGEELGMDIKQKLGLEQTLESIRIVRRKXVIAQTDTYKKLKSTREYRALIHE 167
DB 114 YIGDELESISTEIKQNLQDLTSLKHIRSRKQMLMESLNHLQREKEILENSMLAQ 173
QY 168 LDMKE-----ENPNYGFNV-----ENOSRIYENSIPMN 196
DB 174 IRRRESILRTHQNSFOQNRSHHVAPOPQPLNPYMASSPFLN 216

RESULT 12

US-09-149-976-12
Sequence 12, Application US/09149976
Patent No. 6127123

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-149-976-12

Query Match 27.4%; Score 323; DB 3; Length 251;
Best Local Similarity 37.2%; Pred. NO. 4,9e-24;
Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIEPTNROVYTSKRVRGILKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
DB 1 MGRGKIEIKKIEPTNROVYTSKRVRGILKKAKELTVLCDAOVSLIMFSSGKLADYCSF 60
QY 61 STDIDGI--YERYQV-----VTGMDLMAQYEROMNTLKHINEINOLKREIRR 107
DB 61 SCMEKYLEHYERYVAEKQKLVPSHVAQAQTMSVEYSRLKAKTE-LLENNQ-----RH 113
QY 108 RGEELGMDIKQKLGLEQTLESIRIVRRKXVIAQTDTYKKLKSTREYRALIHE 167
DB 114 YIGDELESISTEIKQNLQDLTSLKHIRSRKQMLMESLNHLQREKEILENSMLAQ 173
QY 168 LDMKE-----ENPNYGFNV-----ENOSRIYENSIPMN 196
DB 174 IRRRESILRTHQNSFOQNRSHHVAPOPQPLNPYMASSPFLN 216

RESULT 13

US-09-398-326-12
Sequence 12, Application US/09398326
Patent No. 635863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 3739
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-398-326-12

Query Match 27.4%; Score 323; DB 3; Length 251;
 Best Local Similarity 37.2%; Pred. No. 4.9e-24;

Matches 83; Conservative 37; Mismatches 69; Indels 34; Gaps 6;

QY 1 MGRGKIEIKKIENPTNRQVYTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGKLADYCSF 60
 DB 1 MGRGVEMKRIENKINQVTFKRRAGLLKKAHEISILCDAEVSLVFSKGLFEYSSE 60
 QY 61 STDIKGI--YERYQV-----VTGMDLNAQYERMONTLKLHNEINONLRKEIRR 107
 DB 61 SCMEKYLEHYERYSYAEKOLKVPDSHNAQTNNVSVEYSRLKAKIE-LLEENQ-----RH 113
 QY 108 RKEEELGMDIKQLRGLEQTLSESLRIVRRKHYVIAOTDTYKKLSTRETYRALIHE 167
 DB 114 YLGEDELSISIKELQNLQOQLDLSLKIRSRKQOLMESGNHQLRKEKEILEENSLAKQ 173
 QY 168 LDKKE-----ENPNYGFNV---ENQSIYENSIPMN 196
 DB 174 IRRRESILRTHQNSEQONSHHVAPOPOPQALNPYMASSPFLN 216

RESULT 14

US-09-410-464-16
 Sequence 16, Application US/09410464
 Patent No. 6395892
 GENERAL INFORMATION:
 APPLICANT: Straubs et al.
 TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 TITLE OF INVENTION: poplar and other plant species.
 FILE REFERENCE: 53375
 CURRENT APPLICATION NUMBER: US/09/410,464
 CURRENT FILING DATE: 1999-10-01
 EARLIER APPLICATION NUMBER: 09/287,700
 EARLIER FILING DATE: 1999-04-06
 EARLIER APPLICATION NUMBER: 60/080,851
 EARLIER FILING DATE: 1998-04-06
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 16
 LENGTH: 238
 TYPE: PRT
 ORGANISM: Populus balsamifera subsp. trichocarpa
 US-09-410-464-16

Query Match 27.4%; Score 322; DB 3; Length 238;
 Best Local Similarity 37.1%; Pred. No. 5.8e-24;

Matches 85; Conservative 43; Mismatches 69; Indels 32; Gaps 9;

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 DB 16 LGRGKYEIKKIENPTNRQVTFCKRRAGLLKKAHEISVLCDAEVALVFSRGLFEYSNN 75
 QY 61 STDIKGIYERYQVTVT-----GMDLNAQYERMONTLKLHNEINONLRKEIRRRGEEL 113
 DB 76 S--VKSTIIEYKACADSSNNGSVSEANAOFYQ-QEAKARSOQG-NLQNSNRMLGESEL 131
 QY 114 EGMIDIKQLRGLEQTLSESLRIVRRKHYVIAOTDTYKKK---LKSTRETYRALIHELD 170
 DB 132 SALSVKELSLKLEIKGIGIRIRSKKNELLFAIEIYVQKREIDLHNHNNQALRAKIAENR 191

QY 171 KEENPNY---GENVE-----NOSRIYENSIPMVECP---OMFS 203
 DB 192 KROHNMIMPEGVNFETMQSOPFDSRNYOV--NGLPANHYPHEDQLFS 238

RESULT 15

US-08-592-214A-8
 Sequence 8, Application US/08592214A
 Patent No. 5811536
 GENERAL INFORMATION:
 APPLICANT: Yanofsky, Martin F.
 TITLE OF INVENTION: Cauliflower Floral Meristem Identify
 TITLE OF INVENTION: Genes and Methods of Using Same
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 City: San Diego
 STATE: California
 COUNTRY: United States
 Zip: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/592,214A
 FILING DATE: 26-JAN-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 1927
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 273 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-592-214A-8

Query Match 27.2%; Score 320; DB 2; Length 273;
 Best Local Similarity 38.6%; Pred. No. 1.1e-23;
 Matches 71; Conservative 44; Mismatches 51; Indels 18; Gaps 3;

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 DB 1 MGRGKIQVKRIENKINQVTFKRRAGLLKKAHEISVLCDAEVALVFSRGLFEYATD 60
 QY 61 STDIKGI--YERYQVTVGMDL-----WNAQYERMONTLKLHNEINONLRKEIRRR 109
 DB 61 SRMDKILERYERYSYAEKALISAESEEGNWCHEYRKLAKKIEFTIOCHGHL-----M 113
 QY 110 GEELEGMIDIKQLRGLEQTLSESLRIVRRKHYVIAOTDTYKKKLSSTRETYRALIHELD 169
 DB 114 GEDLESINPELEQLOQLDSDLSLKIRSRKSHLMASISBELQKERSLQENNALQKELA 173
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 DB 174 ERQK 177

Search completed: January 27, 2005, 13:22:56
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 13:15:34 ; Search time 144 Seconds
(without alignments)
569.533 Million cell updates/sec

Title: US-10-690-246-2

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Scoring table: BLOSUM62
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Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /cgn2_6/prodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177	100.0	227	US-10-690-246-2	Sequence 2, Appli
2	802.5	68.2	224	US-10-690-246-6	Sequence 6, Appli
3	758.5	64.4	222	US-10-690-246-4	Sequence 4, Appli
4	755	64.1	219	US-10-690-246-8	Sequence 8, Appli
5	611	51.9	227	US-10-104-580-4	Sequence 4, Appli
6	556.5	47.3	227	US-10-424-599-263636	Sequence 263636
7	529.5	45.0	223	US-10-425-114-42492	Sequence 42492, A
8	502	42.7	224	US-10-424-599-263637	Sequence 263637, A
9	496	42.1	223	US-10-856-499-601	Sequence 601, App
10	487.5	41.4	186	US-10-437-963-132081	Sequence 132081, A
11	485	41.2	241	US-10-425-114-44825	Sequence 44825, A
12	472	40.1	243	US-10-424-599-209491	Sequence 209491, A
13	471.5	40.1	260	US-10-425-114-39286	Sequence 39286, A

14	462	39.3	261	US-10-425-114-46248	Sequence 46248, A
15	438	37.2	143	US-10-425-114-41663	Sequence 41663, A
16	435	35.3	208	US-10-739-930-8744	Sequence 8744, Ap
17	413	35.1	208	US-10-424-599-208168	Sequence 208168, A
18	413	35.0	209	US-10-425-114-40799	Sequence 40799, A
19	400	34.0	208	US-10-412-6998-56	Sequence 56, Appl
20	387.5	32.9	207	US-10-424-599-175060	Sequence 175060, A
21	381	32.4	205	US-10-425-114-39944	Sequence 39944, A
22	367	31.2	228	US-10-425-114-66169	Sequence 66169, A
23	363.5	30.9	259	US-10-425-115-275777	Sequence 275777, A
24	358	30.4	260	US-10-437-963-113197	Sequence 113197, A
25	354	30.1	195	US-10-856-499-2119	Sequence 2119, Ap
26	353.5	30.0	240	US-09-970-624-2	Sequence 2, Appli
27	353.5	30.0	240	US-10-425-115-340655	Sequence 340655, A
28	351	29.8	235	US-10-437-963-120368	Sequence 120368, A
29	344	29.2	108	US-10-856-499-2182	Sequence 2182, Ap
30	341.5	29.0	255	US-09-853-450-10	Sequence 10, Appl
31	341.5	29.0	255	US-10-794-923-10	Sequence 10, Appl
32	339	28.8	190	US-10-425-114-39581	Sequence 39581, A
33	335	28.5	190	US-10-425-114-40296	Sequence 40296, A
34	333	28.3	246	US-10-259-165-46	Sequence 46, Appl
35	333	28.3	246	US-10-259-165-416	Sequence 416, Appl
36	327	27.8	234	US-09-819-142-16	Sequence 16, Appl
37	327	27.8	234	US-09-934-455-358	Sequence 358, App
38	326	27.7	245	US-10-310-154-614	Sequence 614, App
39	323	27.4	232	US-10-767-701-43179	Sequence 43179, A
40	323	27.4	251	US-09-853-450-12	Sequence 12, Appl
41	323	27.4	251	US-10-794-923-12	Sequence 12, Appl
42	322.5	27.4	281	US-10-425-115-363312	Sequence 363312, A
43	322	27.4	238	US-10-104-580-16	Sequence 16, Appl
44	322	27.4	270	US-10-105-021-2	Sequence 2, Appli
45	321	27.3	253	US-10-767-701-34344	Sequence 34344, A

ALIGNMENTS

RESULT 1	US-10-690-246-2	US-10-690-246-2
1	Sequence 2, Application US/10690246	
2	Publication No. US20040210967A1	
3	GENERAL INFORMATION:	
4	APPLICANT: CHEN, HONG-HWA	
5	INVENTOR: TSAI, WEN-CHIEH	
6	TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID	
7	FILE REFERENCE: U 014863-8	
8	CURRENT APPLICATION NUMBER: US/10/690,246	
9	CURRENT FILING DATE: 2003-10-21	
10	PRIOR APPLICATION NUMBER: 091125320	
11	PRIOR FILING DATE: 2002-10-25	
12	NUMBER OF SEQ ID NOS: 24	
13	SOFTWARE: PatentIn version 3.2	
14	SEQ ID NO 2	
15	LENGTH: 227	
16	TYPE: PRT	
17	ORGANISM: Phalaenopsis equestris	
18	US-10-690-246-2	
19	Query Match	100.0%; Score 1177; DB 17; Length 227;
20	Best Local Similarity	100.0%; Pred. No. 3.6e-99;
21	Matches	227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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32	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
33	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
34	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
35	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
36	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
37	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
38	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
39	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
40	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
41	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
42	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
43	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
44	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60
45	1 MGRGKIKIKIENPTNRQYTSSRRVGIKKAKELTVLCDAQVSLIMFSTGKLADYCS	60

QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227

RESULT 2
 US-10-690-246-6
 / Sequence 6, Application US/10690246
 / Publication No. US20040210967A1
 / GENERAL INFORMATION:
 / APPLICANT: CHEN, HONG-HWA
 / APPLICANT: TSAI, MEN-CHIEH
 / TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 / FILE REFERENCE: U 014863-8
 / CURRENT APPLICATION NUMBER: US/10/690, 246
 / PRIOR FILING DATE: 2003-10-21
 / PRIOR APPLICATION NUMBER: 091125320
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 6
 / LENGTH: 224
 / TYPE: PRF
 / ORGANISM: Phalaenopsis equestris
 US-10-690-246-6

Query Match 68.2%; Score 802.5; DB 17; Length 224;
 Best Local Similarity 65.2%; Pred. No. 5, 4e-65;
 Matches 148; Conservative 47; Mismatches 29; Indels 3; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 Db 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 QY 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 180
 Db 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 180
 QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 181 EDSSN--YEGVALANDSGSHMYAFR-VQPNQONLQGTGYSHDLRKA 224

RESULT 3
 US-10-690-246-4
 / Sequence 4, Application US/10690246
 / Publication No. US20040210967A1
 / GENERAL INFORMATION:
 / APPLICANT: CHEN, HONG-HWA
 / APPLICANT: TSAI, MEN-CHIEH
 / TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 / FILE REFERENCE: U 014863-8
 / CURRENT APPLICATION NUMBER: US/10/690, 246
 / PRIOR FILING DATE: 2003-10-21
 / PRIOR APPLICATION NUMBER: 091125320
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 4
 / LENGTH: 222
 / TYPE: PRF
 / ORGANISM: Phalaenopsis equestris
 US-10-690-246-4

Query Match 64.4%; Score 758.5; DB 17; Length 222;
 Best Local Similarity 62.6%; Pred. No. 5, 6e-61;
 Matches 142; Conservative 44; Mismatches 36; Indels 5; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 Db 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 QY 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 180
 Db 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 180
 QY 181 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 227
 Db 177 VDDPNNYDGAALNGASVLYSFR-TQSPQPNLQGTGYSHDLRKA 222

RESULT 4
 US-10-690-246-8
 / Sequence 8, Application US/10690246
 / Publication No. US20040210967A1
 / GENERAL INFORMATION:
 / APPLICANT: CHEN, HONG-HWA
 / APPLICANT: TSAI, MEN-CHIEH
 / TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
 / FILE REFERENCE: U 014863-8
 / CURRENT APPLICATION NUMBER: US/10/690, 246
 / PRIOR FILING DATE: 2003-10-21
 / PRIOR APPLICATION NUMBER: 091125320
 / NUMBER OF SEQ ID NOS: 24
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 8
 / LENGTH: 219
 / TYPE: PRF
 / ORGANISM: Phalaenopsis equestris
 US-10-690-246-8

Query Match 64.1%; Score 755; DB 17; Length 219;
 Best Local Similarity 66.5%; Pred. No. 1, 1e-60;
 Matches 149; Conservative 36; Mismatches 29; Indels 10; Gaps 2;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 Db 1 MGRGKIEIKKIENPTNRQVTSKRRVGLKKAKELTVLCDAQVSLIMFSSGTGLADYCSF 60
 QY 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 Db 61 STDIKGIYERYQVVTGMDLMAQYERMONTLKHLNEINONLRKEIRRKGEELGMDIKQ 120
 QY 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 179
 Db 121 LRGLQTLLESRLRYHRKRYHVIATQDTYKKKLSRETYRALIHELDMEENPNYGFN 179
 QY 180 VENOSRIYENSIPWNECPQMFSPRVVHPNPNLGLGYESHDLSTA 223
 Db 181 LVEDLSCTYDSSISMANR-----LHSEPNVQVVECHRE 215

RESULT 5
 US-10-104-580-4
 / Sequence 4, Application US/10104580
 / Publication No. US2003003628A1
 / GENERAL INFORMATION:
 / APPLICANT: Straus et al.
 / TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
 / FILE REFERENCE: 62486
 / CURRENT APPLICATION NUMBER: US/10/104,580
 / PRIOR FILING DATE: 2002-03-21
 / PRIOR APPLICATION NUMBER: 09/410,464
 / PRIOR FILING DATE: 1999-10-01
 / PRIOR APPLICATION NUMBER: 09/287,700

PRIOR FILING DATE: 1999-04-06
 PRIOR APPLICATION NUMBER: 60/080,851
 PRIOR FILING DATE: 1998-04-06
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 4
 LENGTH: 227
 TYPE: PRT
 ORGANISM: Populus balsamifera subsp. trichocarpa
 US-10-104-580-4

Query Match 51.9%; Score 611; DB 14; Length 227;
 Best Local Similarity 55.2%; Pred. No. 1.7e-47;
 Matches 128; Conservative 36; Mismatches 56; Indels 12; Gaps 4;

QY 1 MGRGKIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
 QY 61 STDIKGIYERYVVTGMDLNAQYERMQNTLKLHNEINQNLKREIRRKGEELGMDIKQ 120
 DB 61 STSTKKIYQYQNALGIDLMGTQYERKQEHRLKRLNDINHLRQEIQRORGEGLNDLSIDH 120
 QY 121 LRGLEQTLSESLRIVRHARKYHVIATQDTYKKLKSRETRYRLIHLELDMKEENPNYGFN 180
 DB 121 LRGLEQTHMTEALGVGRKTHVKTQNEYRKVKVKNLEEHGMLHEYEAKLEDROQGL- 179
 QY 181 VENQSRISYENSIPMNECPQMFSPRVVHPNQ-----PNT-LGLGYESHDLSTL 226
 DB 180 VDN-----EAAVALANGASNLVAFRLHGHNNHHLPNLHLGDFGFAHLEURL 226

RESULT 6
 US-10-424-599-263636
 ; Sequence 263636, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 263636
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80083C.1.pep
 ; US-10-424-599-263636

Query Match 47.3%; Score 556.5; DB 15; Length 227;
 Best Local Similarity 50.7%; Pred. No. 1.6e-42;
 Matches 108; Conservative 44; Mismatches 58; Indels 3; Gaps 3;
 QY 1 MGRGKIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
 DB 1 MGRGKIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSF 60
 QY 61 STDIKGIYERYVVTGMDLNAQYERMQNTLKLHNEINQNLKREIRRKGEELGMDIKQ 120
 DB 61 STSTKKIYQYQNALGIDLMGTQYERKQEHRLKRLNDINHLRQEIQRORGEGLNDLSIDH 120
 QY 121 LRGLEQTLSESLRIVRHARKYHVIATQDTYKKLKSRETRYRLIHLELDMKEENPNYGFN 180
 DB 121 LRGLEQTHMTEALGVGRKTHVKTQNEYRKVKVKNLEEHGMLHEYEAKLEDROQGL- 179
 QY 181 VENQSRISYENSIPMNECPQMFSPRVVHPNQPN 213

DB 180 IDNGGE-YESVIGFSNLGPRMFALS-LQPSHP 210

RESULT 7
 US-10-425-114-42492
 ; Sequence 42492, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 42492
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700958586_FLI.pep
 ; US-10-425-114-42492

Query Match 45.0%; Score 529.5; DB 15; Length 223;
 Best Local Similarity 49.3%; Pred. No. 4.5e-40;
 Matches 103; Conservative 45; Mismatches 58; Indels 3; Gaps 3;

QY 5 KIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSFSTDI 64
 DB 1 KIEIKKIEPTNRQVYTSKRVRGILKKAKELTVLCAQVSLIMFSSTGKLADYCSFSTDI 60
 QY 65 KGIYERYVVTGMDLNAQYERMQNTLKLHNEINQNLKREIRRKGEELGMDIKQ 124
 DB 61 KQFDDYQNTLGVLDLNSHYENQNLKRLKDVNRRLKREIRKRWGDCIADLGMEDKCL 120
 QY 125 EQLTEESLRIVRHARKYHVIATQDTYKKLKSRETRYRLIHLELDMKEENPNYGFVNO 184
 DB 121 EEMDMQAAVYERKTKVITNQIDTQKFFNEKEVHNRLLRDLRADPRFAL-IDNG 179
 QY 185 SRIYENSIPMNECPQMFSPRVVHPNQPN 213
 DB 180 GE-YESVIGFSNLGPRMFALS-LQPSHP 206

RESULT 8
 US-10-424-599-263637
 ; Sequence 263637, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 263637
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_80084C.1.pep
 ; US-10-424-599-263637

Query Match 42.7%; Score 502; DB 15; Length 234;

Best Local Similarity 46.0%; Pred. No. 1.6e-37;
Matches 103; Conservative 45; Mismatches 58; Indels 18; Gaps 5;

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QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MARGKIQIKRIENTNRQVYTSKRNGLFKKANELTVLCDAKAVSLIMFSSGTGLHEYIS 60
QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIKQ 120
DB 61 STSTRQFDDQYQMTLGVLMNSHYENMOENLKKLDVNRMLRKEIRORMGDCINDLGMD 120
QY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENP 176
DB 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENP 176
QY 170 MKEENPNYGFVENQSRIVENSIPMVNECPQMSFRVHNOGN 213
DB 177 ARADPRAL-IDNGGE-YESVIGFSMLGPRMFLS-LQPSHPS 217

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RESULT 9

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US-10-856-499-601
/ Sequence 601, Application US/10856499
/ Publication No. US20040259145A1
/ GENERAL INFORMATION:
/ APPLICANT: Wood, Marion
/ APPLICANT: Shenk, Michael A.
/ APPLICANT: McGrath, Annette
/ TITLE OF INVENTION: Compositions and Methods for the
/ FILE REFERENCE: 11000.1021C2
/ CURRENT APPLICATION NUMBER: US/10/856,499
/ NUMBER OF SEQ ID NOS: 2370
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 601
/ LENGTH: 233
/ TYPE: PRT
/ ORGANISM: EucaIyptus grandis
US-10-856-499-601

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Query Match 42.1%; Score 496; DB 17; Length 233;
Best Local Similarity 46.2%; Pred. No. 5.5e-37;
Matches 104; Conservative 46; Mismatches 65; Indels 10; Gaps 5;

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QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MARGKIQIKRIENTNRQVYTSKRNGLFKKANELTVLCDAKAVSLIMFSSGTGLHEYIS 60
QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIKQ 120
DB 61 STSTRQFDDQYQMTLGVLMNSHYENMOENLKKLDVNRMLRKEIRORMGDCINDLGMD 120
QY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENP 175
DB 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENP 175
QY 176 MKEENPNYGFVENQSRIVENSIPMVNECPQMSFRVHNOGN 218
DB 181 HFGM-VDN-GRDYEAIVGYTDAARAAARLYTLR-LQPDQNLTSGG 222

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RESULT 10

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US-10-437-963-132081
/ Sequence 132081, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei

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/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 132081
/ LENGTH: 186
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_34084C.1.pap
US-10-437-963-132081

```

Query Match 41.4%; Score 487.5; DB 16; Length 186;
Best Local Similarity 48.5%; Pred. No. 2.4e-36;
Matches 110; Conservative 32; Mismatches 42; Indels 43; Gaps 8;

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QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 1 MARGKIEIKRIENATNRQVYTSKRRTGIMKKARELTVLCDAQVAILMFSSGT-----52
QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKLNEINONIRKEIRRRKGEELGMDIKQ 120
DB 53 -NIGDIPRYQQAIGTSLMIEQ-----ORMGEDLDGLEFDE 87
QY 121 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENPNYGF 180
DB 88 LRGLQTLLESIRIVRRKHVIAOTDTYKKKLKSTRETYRALIHE-----LDMKEENPNYGF 180
QY 181 VENQSRIVENSIPMVNECPQMSFRVHNOGN 226
DB 141 VDNQGGWDGAG-AGAAADWFAFRV-PSQPNLHGMAYGNNHDLRL 185

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RESULT 11

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US-10-425-114-44825
/ Sequence 44825, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(5313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 44825
/ LENGTH: 241
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 701209467_F1.pap
US-10-425-114-44825

```

Query Match 41.2%; Score 485; DB 15; Length 241;
Best Local Similarity 46.2%; Pred. No. 5.8e-36;
Matches 110; Conservative 38; Mismatches 74; Indels 16; Gaps 5;

```

QY 1 MGRGKIEIKIENPTNRQVYTSKRVRGILKKAKELTVLCDAQVSLIMFSSGTGLADYCS 60
DB 9 MARGKIEIKIENPTNRQVYTSKRNGLFKKANELTVLCDAKAVSLIMFSSGTGLHEYIS 68
QY 61 STDIGIYERYQVVTGMDLMAQYERMONTLKLNEINONIRKEIRRRKGE--ELEGM 117

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Db 69 GLTTKRIIDQYQTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGIDMDMS 128
QY 118 IKOLRGLEQTLSESLIRVRHKYHVIATOTDTYKKKLSKSTREYRALIHELDMKEENPNY 177
Db 129 FOQLRTLEEDLVSSIGIKIRKRFHVITKRTDCKRKVKSLEQNMRLDLELEKCAIHPQF 188
QY 178 GFNVENQSRIVYENSIMWNECPMFSPRVVHPNQPNLIGGYESH-----DLSLA 227
Db 189 ILHDEGDE---BSAVNALANGASTLVAFCHQHSHLNL-PSHSHSGEPPKTDLDRLA 241

RESULT 12

US-10-424-599-209491
Sequence 209491, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209491
LENGTH: 243
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_31198C.1.pep
US-10-424-599-209491

Query Match 40.1%; Score 472; DB 15; Length 243;
Best Local Similarity 45.3%; Pred. No. 9e-35;
Matches 111; Conservative 40; Mismatches 74; Indels 20; Gaps 7;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60
Db 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60
QY 61 STDIKIYERYQVVTG-MDLMAQYERMONTLKHLNEINONLKEIRRRKGE--ELEGMD 117
Db 61 GLTTKRIIDQYQTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGIDMDMS 120
QY 118 IKOLRGLEQTLSESLIRVRHKYHVIATOTDTYKKKLSKSTREYRALIHELDMKEE---N 174
Db 121 FOQLRTLEEDLVSSIGIKIRKRFHVITKRTDCKRKVKSLEQNMRLDLELEKCAIHPQF 178
QY 175 PNYGF---NVENQSRIVYENSIMWNECPMFSPRVVHPNQPNL---GLGYE-----SH 222
Db 179 PGFLHDEGDEBSAALAAVALANGASTLVAFCHQHSHLNLFSHNSGGEQPFKTDH 238
QY 223 DLSLA 227
Db 239 DLRLA 243

RESULT 13

US-10-425-114-39286
Sequence 39286, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou Yihua
APPLICANT: Kovalic David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 39286
LENGTH: 260
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3049-050-fE_FLI.pep
US-10-425-114-39286

Query Match 40.1%; Score 471.5; DB 15; Length 260;
Best Local Similarity 44.6%; Pred. No. 1.e-34;
Matches 108; Conservative 41; Mismatches 78; Indels 15; Gaps 5;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60
Db 19 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 78
QY 61 STDIKIYERYQVVTG-MDLMAQYERMONTLKHLNEINONLKEIRRRKGE--ELEGMD 117
Db 79 GLTTKRIIDQYQTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGIDMDMS 138
QY 118 IKOLRGLEQTLSESLIRVRHKYHVIATOTDTYKKKLSKSTREYRALIHELDMKEENPNY 177
Db 139 FOQLRTLEEDLVSSIGIKIRKRFHVITKRTDCKRKVKSLEQNMRLDLELEKCAIHPQF 198
QY 178 GF---NVENQSRIVYENSIMWNECPMFSPRVVHPNQPNL---GLGYE-----SHLS 225
Db 199 ILHDEGDEBSAALAAVALANGASTLVAFCHQHSHLNLFSHNSGGEQPFKTDHDLR 258
QY 226 LA 227
Db 259 LA 260

RESULT 14

US-10-425-114-46248
Sequence 46248, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou Yihua
APPLICANT: Kovalic David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46248
LENGTH: 261
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: 701148021_FLI.pep
US-10-425-114-46248

Query Match 39.3%; Score 462; DB 15; Length 261;
Best Local Similarity 44.1%; Pred. No. 8.1e-34;
Matches 108; Conservative 43; Mismatches 74; Indels 20; Gaps 7;

QY 1 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 60
Db 19 MGRGKIEIKKIENPTNRQVTSKRRVGIKKAKELTVLCDAQVSLIMFSSTGLADYCSF 78
QY 61 STDIKIYERYQVVTG-MDLMAQYERMONTLKHLNEINONLKEIRRRKGE--ELEGMD 117
Db 79 GLTTKRIIDQYQTLGDIDIMSHYKMLENLKLDINNKLRQIRHRIGEGIDMDMS 138

[illegible]

```

SEQUENCE 2
US-09-410-464-3
/ Sequence 3, Application US/09410464
/ Patent No. 6395892
/ GENERAL INFORMATION:
/ APPLICANT: Strauss et al.
/ TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
/ TITLE OF INVENTION: poplar and other plant species.
/ FILE REFERENCE: 53375
/ CURRENT APPLICATION NUMBER: US/09/410,464
/ CURRENT FILING DATE: 1999-10-01
/ EARLIER APPLICATION NUMBER: 09/287,700
/ EARLIER FILING DATE: 1999-04-06
/ EARLIER APPLICATION NUMBER: 60/080,851
/ EARLIER FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 681
/ TYPE: DNA
/ ORGANISM: Populus balsamifera subsp. trichocarpa
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(681)
US-09-410-464-3

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Query Match	24.8%	Score 227.2;	DB 3;	Length 681;
Best Local Similarity	58.4%;	Pred. No. 2.2e-52;		
Matches 397;	Conservative 0;	Mismatches 283;	Indels 0;	Gaps 0

vY 76 ATGGGGAGGGGAAAGATAGAGATATAAAAAAGATAGGAATCCGACGAACAGCAAGTACA 135
 Db 1 ATGGGCTGTGGAAAGATGAAATCAAGAAAGATCGAAAAATCCCAAAACAGGCAAGTACCC 60
 QY 136 TAATCTTAAGAGAGAGAGTGGGATTACTCAAGAAAGGCCAAGAGCTCACTGTCTCTGTGAT 195
 Db 61 TACTCGAAGGAAGAAATGTAATTTTCAAGAAAGCCCAAGAACTCACTGACTTTGTAT 120
 QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGCAACAGAAAGTTGGCTGATTCTGACAGCCCC 255
 Db 121 GCTAAAGTCTCTTATCATGATTTCTCCAACTCAACAACTCATATGATGATTAACCCCC 180
 QY 256 TCTACTGATTAATTAAGGGATATATGAGAGATCAACGAGTTGTGACTGAAATGATCTATGG 315

Db	181	TCACATCGACMAAAGAAATCTACGATCAATATCAGAAACGCTTTAGGCATGATCTCTGG	240
Qy	316	AATGCTCAGATATGAGAGATGCGAATAAGCCTGAAGATTTGAATGAGATTAACCAAAAC	375
Db	241	GGCACTCAATATCGAGAAATATGCAAGAGCACTTGAGAGAGCTGAATGATATCAATCTATAG	300
Qy	376	CTGAGAGAGAGATTAGAGAGAGAAAGGGAGAAATTGAGAGGCATGCAATMAAGCA	435
Db	301	CTGAGACMAAATAATCAGGCAGAGAGAGAGAGAGGCGCTGAATGATCTGAGCATTTGATCAT	360
Qy	436	CTGCGCGCTCTTGAGAAACTTTGAGAAAGTCTCTTGAATTTGTTGCGATGAAAGTAT	495
Db	361	CTGCGCGGCTTTGAGCACTATGACTGAACCTTTGAATGATGTGGTGGCGAGGAAGTATC	420
Qy	496	CATGATATGCCACACAAACTGACACTTACAAAGAAAGCTTAAAAAGCACAAGGGAAACT	555
Db	421	CATGATATPAAAAACMAAACAAACCTTACAGAGAAAGGTGAAGATTTTAAGAGAGACA	480
Qy	556	TACCGCGCTCTAATCATGAATGGATGTATGAAAGAGAGAACTCCAACTACGGTTTTAAT	615
Db	481	CATGGAACCTCTTATATGAAATATATAGCAAACTAGAGAGATCGACAAATATGTTTTAGTG	540
Qy	616	GTAGAAAAACAGATGAAATTTATGAAAAATTCGATTCCAATGATGTAATGATGCTCTCAG	675
Db	541	GACAAATGAGCTGCTGTTGCACTTGCAATGAGGGGCTTCCAACTCTATGCAATTCGCGCTG	600
Qy	676	ATGTTTTCTTTAGGGGTGTTCAATCCGAATAGCCCAATCTGCTTGGTTTATAGTTATGAA	735
Db	601	CATCAGCGGACAAACACACACCACTCATCTCTTAATCTTACCTTGAGAGATGATTTGGA	660
Qy	736	TCATCATATCTTAACTTGC	755
Db	661	GCCCATGAACCTTGCCTTCC	680

```

RESULT 3
US-09-410-464-1
; Sequence 1, Application US/09410464
; Patent No. 6395892
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral
; FILE REFERENCE: 53375
; CURRENT APPLICATION NUMBER: US/09/410,464
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 09/287,700
; EARLIER FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,851
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4285
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-1

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Query Match	11.9%	Score 109.4;	DB 3;	Length 4285;
Best Local Similarity	73.3%	Pred. No. 7.5e-20;		
Matches 140; Conservative	0.0	Mismatches		

	Sequence	Match	Indels	Gaps
OY	70 AGAGAGATGGGAGGGCGGAGATGAGATGAAAAAGATAGAGATCCGACGAACGGCA	129	0	0
Db	1995 AAAAATATGGGCTGGGAAATGGAAATCAAGAGATGAAAAACCCCAACAAACGGCA	2054	0	0
OY	130 GTTACATATTTCAAGAGAGATTGGATCTGAAAGGCCAAGAGATCTGTGTTTC	189	0	0
Db	2055 GTCACCTACTCCAGAGAGAAATGGATTTTCAABAAAGCCCAAGAACTACGTACTTT	2114	0	0
OY	190 TGTGATGCTCAGGCTCTCTTCATCATGTTTCTCAAGCAACGAAAGTTGGCTGATTATGTC	249	0	0
Db	2115 TGTGATGCTAAGCTCTCTCTTTATCATGTTCTCCAAACACTCAACAACTCAATGAATACATT	2174	0	0

QY 250 AGCCCTCTAC 260
DB 2175 AGCCCTCCAC 2185

RESULT 4

US-08-867-087B-16

; Sequence 16, Application US/08867087B

; Patent No. 5990386

; GENERAL INFORMATION:

; APPLICANT: An. Gynheung

; TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT

; TITLE OF INVENTION: AND APICAL DOMINANCE IN PLANTS

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell Leigh &

; ADDRESSEE: Whinston, LLP

; STREET: One World Trade Center

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3-1/2 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/867, 087B

; FILING DATE: June 2, 1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/323,449

; FILING DATE: October 14, 1994

; APPLICATION NUMBER: U.S. 08/485,981

; FILING DATE: June 7, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Alan. E.

; REGISTRATION NUMBER: 35,123

; REFERENCE/DOCKET NUMBER: 4630-47071

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1180 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

US-08-867-087B-16

Query Match 11.1%; Score 101.8; DB 2; Length 1180;
Best Local Similarity 65.8%; Pred. No. 4,7e-18;
Matches 148; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 28 GAAGGTTGAGACAGAGGAAAAGGAGGAGAAAGAGAGATGGGAGAGGCG 87
DB 62 GAGCCGCGTGAAGTGAAGTGAAGAGAGAGAGAGAGATCGGATGGGAGAGG 121
QY 88 AAGATGAGATGAAAAAGATGAGAAATCCGACGAAACAGGCAAGTTATTTTAAAGG 147
DB 122 AGGATGAGATGAAAGAGATCGAAGCAAGATCAACAGGAGGATTCGCGAAGCGG 181
QY 148 AGAGTTGGATATGAAAGAGCCCAAGAGACTCACTGTTCTGTGATGTCTAGGTTCT 207
DB 182 AGGAATGGGCTGCTCAAGAGGCGTACGAGCTCTCCGCTGTGCGAGCGCGAGTCCG 241
QY 208 CTGATGATGTTTCAAGACAGAGAAAGTTGCTGATTAATGACG 252
DB 242 CTCATCATCTTCTCAACCGCGGCAAGCTTACGAGTTCTGACG 286

RESULT 5
US-08-485-981-9
; Sequence 9, Application US/08485981
; Patent No. 5861542

GENERAL INFORMATION:

; APPLICANT: An. Gynheung

; TITLE OF INVENTION: GENE CONTROLLING FLORAL DEVELOPMENT AND

; TITLE OF INVENTION: APICAL DOMINANCE IN PLANTS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klarquist Sparkman Campbell Leigh &

; ADDRESSEE: Whinston

; STREET: One World Trade Center

; STREET: Suite 1600

; CITY: Portland

; STATE: Oregon

; COUNTRY: United States of America

; ZIP: 97204

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Disk, 3-1/2 inch

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,981

; FILING DATE: June 7, 1995

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/323,449

; FILING DATE: October 14, 1994

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Dow, Alan. E.

; REGISTRATION NUMBER: 35,123

; REFERENCE/DOCKET NUMBER: 4630-42933

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (503) 226-7391

; TELEFAX: (503) 228-9446

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 945 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double stranded

; TOPOLOGY: linear

US-08-485-981-9

Query Match 10.7%; Score 98.4; DB 2; Length 945;
Best Local Similarity 70.2%; Pred. No. 3,6e-17;
Matches 132; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 72 AGAGATGGGAGGAGGAGATGAGATGAGTAAAAAGATGAGAAATCCGACGAGGCAAGT 131
DB 12 AAAAATGGAGAGGAGGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 71
QY 132 TACATATTTTAAGAGAGAGGATGAGTGAAGAGGCAAGAGACTGTTCTTG 191
DB 72 GACCTTCGTAAGAGAGAAATGAGACTTTGAAAAAGCTTATGACCTTCTGTTCTTG 131
QY 192 TGATGCTCAAGTCTCTCTATCATGTTTCAAGACAGAGAAAGTTGCTGATTAATGACG 251
DB 132 TGATGCTCAAGTCTCTCTATCATGTTTCAAGTGAAGGAGAAAGTGAAGTTCGACG 191
QY 252 CCCCTCTA 259
DB 192 TAGCTCTA 199
RESULT 6
US-08-867-087B-10
; Sequence 10, Application US/08867087B

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/ Patent No. 5990386
/ GENERAL INFORMATION:
/ APPLICANT: An, Gynheung
/ TITLE OF INVENTION: GENES CONTROLLING FLORAL DEVELOPMENT
/ NUMBER OF INVENTION: AND APICAL DOMINANCE IN PLANTS
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Klarquist Sparkman Campbell Leigh &
/ ADDRESSEE: Whinston, LLP
/ STREET: One World Trade Center
/ STREET: 121 S.W. Salmon Street
/ CITY: Portland
/ STATE: Oregon
/ COUNTRY: United States of America
/ ZIP: 97204
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Disk, 3-1/2 inch
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: MS DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/867,087B
/ FILING DATE: June 2, 1997
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. 08/323,449
/ FILING DATE: October 14, 1994
/ APPLICATION NUMBER: U.S. 08/485,981
/ FILING DATE: June 7, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dow, Alan E.
/ REGISTRATION NUMBER: 35,123
/ REFERENCE/DOCKET NUMBER: 4630-47071
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (503) 226-7391
/ TELEFAX: (503) 228-9446
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 945 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double stranded
/ TOPOLOGY: linear
/ US-08-867-087B-10

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Query Match
Best Local Similarity 10.7%; Score 98.4; DB 2; Length 945;
Matches 132; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 72 AGAGATGGGAGGGGAGATAGAGATPAAAGATGAGATCCGACCAAGCAAGT
DB 12 AAAAAATGGAGGGGTGGGTGAGCTTAAGAGATAGAGAACAGATCAACAGGCAAGT
QY 132 TACATATTCTAAGAGAGAGTTGGATTAAGAGAGCCAGAGCTCTCTCTCTG
DB 72 GACCTTGCTTAAGAGAGAAATGACTTTGAAAAAGCTTAAGAGCTTTCTGTTCTTG
QY 192 TGATGCTCAGGCTCTCTCATCATGTTTCAAGCAGAGAAAGTTGGCTGATCTCAG
DB 132 TGATGCTCAGGCTCTCTCATCATGTTTCAAGCAGAGAAAGTTGGCTGATCTCAG
QY 252 CCCCTCTA 259
DB 192 TAGCTCTA 199

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/ TITLE OF INVENTION: EXPRESSION OF AGL15 SEQUENCE IN
/ TRANSGENIC PLANTS
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Quarles & Brady
/ STREET: 1 South Pinckney Street
/ CITY: Madison
/ STATE: WI
/ COUNTRY: US
/ ZIP: 53701-2113
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/904,284
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J.
/ REGISTRATION NUMBER: 27,386
/ REFERENCE/DOCKET NUMBER: 960296.94193
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (608) 251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1070 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-904-284-1

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Query Match
Best Local Similarity 10.6%; Score 96.8; DB 3; Length 1070;
Matches 251; Conservative 0; Mismatches 187; Indels 12; Gaps 3;
QY 69 GAGAGAGATGGGAGGGGAGATAGAGATPAAAGATGAGATCCGACCAAGCAAGT
DB 12 GGGGAAATGGGTGGGTGAGCTTAAGAGATAGAGATGAGATGAGATGAGATGAGAT
QY 129 AGTTATATTTTAAAGAGAGAGTTGGATTAAGAGAGCCAGAGCTCTCTCTCTG
DB 72 AGTCACTTTTCCAGAGAGCGTCTGGGTTACTTAAGAAAGCTCGAGAGCTCTGTTCT
QY 189 CTGTATGCTCAGGCTCTCTCATCATGTTTCTCAAGCAGAGAAAGTTGGCTGATCTG
DB 132 TTGTATGCTCAAGTTGCTCTCATCATGTTTCTCTTAAGTCTGCAAGCTCTTCAAGTCTG
QY 249 CAGCCCTCTACTGATATTAAGGAGATATAGAGATGAGATGAGATGAGATGAGATGAGAT
DB 192 CAG-----TACTGAGATGAGCAACACTTCCAGATTC-----GTTATCAACCAAGT
QY 309 TCTATGAGATGCTCAGTATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT
DB 241 TCTTCAAGCTTCTAAACAGAGAGATTTGTGAGAGGTGATATTTAAAGATCAACTT
QY 369 CCAAACTGAGAGAGAGATTTAGAGAGAGAGAGAGAAATTGAGAGGCAATGACAT
DB 301 TCAAAGCTTCAAGAGAAACATTTACA-ACGACAGGCGCAAGGCTTAAATCCTTGAACCTT
QY 429 AAAGCAATCGCGGCTCTTGAAGCAACTTTGGAAGCTCTTGAATTTGATGAGATGAGATGAG
DB 360 TAAAGAGCTGCAAGAGCTTGAAGCAACTTATATCAATGATGATTAATCTGTCAGAGAGG
QY 489 AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
DB 420 AAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,677
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/067,800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2948
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 101..827
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1062
OTHER INFORMATION: /note="There is a poly(A) tail at
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1062
OTHER INFORMATION: /note="Nucleotide and Deduced
Amino Acid Sequences of the AGL8 cDNA clone."
US-09-349-677-1

Query Match
Best Local Similarity 10.5%; Score 96.6; DB 3; Length 1062;
Matches 132; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 68 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 127
DB 93 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 127
QY 128 AAGTACATATCTTAAGAGAGAGATGGAGTACGAGAGAGCCAGAGCTGCTTC 187
DB 153 AAGTACTTCTCAAAAGAGAGGCTGCTTCTCAAGAGAGCTCATGATCTCTGTC 212
QY 188 TCTGTATGCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTGGCTGATTACT 247
DB 213 TCTGTATGCTCAGGCTCTCTCATCATGTTCTCTTCTCAAGAGCAAACTCTCGAATATT 272
QY 248 GCAGCCCTCT 258
DB 273 CCACCGACTCT 283

RESULT 11
US-09-708-584-1
Sequence 1, Application US/09708584
Patent No. 6541683
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Marijnsen, Robert
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Method of Increasing Fruit Size in a Plant
FILE REFERENCE: P-UD 3040
CURRENT APPLICATION NUMBER: US/09/708,584
CURRENT FILING DATE: 2000-11-07
PRIOR APPLICATION NUMBER: 09/105,652
PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/051,030
PRIOR FILING DATE: 1997-06-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 1
LENGTH: 1062
TYPE: DNA
ORGANISM: Arabidopsis sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(826)
NAME/KEY: polyA_signal
LOCATION: (1061)
US-09-708-584-1

Query Match
Best Local Similarity 10.5%; Score 96.6; DB 4; Length 1062;
Matches 132; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 68 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 127
DB 93 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 152
QY 128 AAGTACATATCTTAAGAGAGAGTGGATACGAGAGCCAGAGCTGCTTC 187
DB 153 AAGTACTTCTCAAAAGAGAGGCTGCTTCTCAAGAGAGCTCATGATCTCTGTC 212
QY 188 TCTGTATGCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTGGCTGATTACT 247
DB 213 TCTGTATGCTCAGGCTCTCTCATCATGTTCTCTTCTCAAGAGCAAACTCTTGAATATT 272
QY 248 GCAGCCCTCT 258
DB 273 CCACCGACTCT 283

RESULT 12
US-09-981-087A-1
Sequence 1, Application US/09981087A
Patent No. 6768042
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Liljegren, Sarah
APPLICANT: Ferrandiz, Cristina
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
FILE REFERENCE: 19452A-000940US
CURRENT APPLICATION NUMBER: US/09/981,087A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 1062
TYPE: DNA
ORGANISM: Arabidopsis sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (101)..(829)
OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-981-087A-1

Query Match
Best Local Similarity 10.5%; Score 96.6; DB 4; Length 1062;
Matches 132; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 68 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 127
DB 93 AGAGAGATGGGAGGAGGAGATAGATATAAAGATAGAGATCCGACGACGCG 152
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0 , Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,284
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-904-284-2

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Query Match	10.1%	Score 93;	DB 3;	Length 795
Best Local Similarity	53.8%;			
Matches 245; Conservative	0;	Mismatches 195;		Indels

16 ATGGGAGGGGGAAGATAGATATAAAAGATGAGAAATCCGACGAACAGCAAGTTACA 135
1 ATGGGTCGTGGAAAAATTGAGATTAAGATGAGATTCGAATTCGAATGACAGGCAAGTTACC 60
136 TATTCTAAGAGAGAGATTGGGATATCTGAAGAAAGCCCAAGAGCTCACTTTCTGTGAT 195
61 TTCTCAAGAGGCGTCTGTGTTGTCTCAAAAAGCTCAAGAGCTCTGTCTTTGTGAC 120
196 GCTCAGGTCCTCTCATCATGATGTTCTCAAGCAACGAAATGGCTGATTAATCTCAGCCCC 255
121 GCTGAGGTCGCCGTCATGTCCTTCTCCAAGTCGGCAAGCTTTGAAAGTTCTCAAGTACT 180
256 TCTACTGATATTA-----AGGGATATATGAGAGTACAGAGTTGTGACTGGA 303
181 AGCATGAGAAAACATTTTGAGATACGGAATTTACAGATCTCTTGAGATGTTCTCTGG 240
304 ATGAGCTATGGAAGTCTCAGTATGAGAGATGACGAATAGCTGAGACATCTGAATGAG 363
241 AT---TACTGTAAAAACAGAGAACAGAGAGGTGACAGAGTGGACCTTTTAAAGAT 297
364 ATTTAACCAAACTGAGAGAAGAGATTGAGAGAGGAAAGGGAGGAATTTGAGAGGATG 423
238 GAGATCTCAATGCTTCAAGAGAAACATTTACACATGAGAGGTAAAGCCCTTGAACCTTCG 357
424 GACATAAAGCAATCCGCGGCTTGTAGCAAACTTTGAMAGTCTCTTGAATTTGTAGG 483
358 AGCTTGAAGAGCTGGCAACACCTTGAAGAACCACTAAATTTCTCATTTGATTTGTGAGA 417
484 CATGAAGATTCATGTGATGTCGCCACAACAACGA 518
Db GAGGAAAGAACTATTTGATCTAAACAACCTTGA 452

Search completed: February 1, 2005, 23:48:56
Job time : 111 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 18:51:50 ; Search time 3957 Seconds
(Without alignments)
10958.973 Million cell updates/sec

Title: US-10-690-246-1

Perfect score: 917

Sequence: 1 acgcggagacagcagaggaag.....ttttgtttgttttttcgg 917

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	910	99.2	910	8	AY378149	AY378149 Phalaenop
2	359.4	39.2	1030	8	AY378148	AY378148 Phalaenop
3	339.2	37.0	942	8	AY196350	AY196350 Oncidium
4	335	36.5	952	8	AB094964	AB094964 Asparagus
5	324.2	35.4	1028	8	AY378147	AY378147 Phalaenop
6	316.8	34.5	980	8	AY378150	AY378150 Phalaenop
7	304.2	33.2	1005	8	AB071378	AB071378 Lillium re
8	299.4	32.6	1039	8	AF503913	AF503913 Lillium re
9	295.6	32.2	833	8	AF209729	AF209729 Hemerocal
10	292.8	31.9	938	8	AF230706	AF230706 Tacca cha
11	285.4	31.1	651	8	AY337750	AY337750 Eupomatia
12	285.4	31.1	651	8	AY337751	AY337751 Eupomatia
13	284.8	31.1	852	8	AB050649	AB050649 Magnolia
14	282.2	30.8	1002	8	AB094965	AB094965 Tulipa ge
15	265.8	29.0	1016	8	AB094966	AB094966 Tulipa ge
16	264.4	28.7	830	8	AY397762	AY397762 Chloranth
17	263	28.7	1210	8	AB003323	AB003323 Oryza sat
18	263	28.7	1210	8	AK069317	AK069317 Oryza sat
19	261	28.5	896	8	AY627630	AY627630 Akebia tr

20	260	28.4	1061	8	AF077760	AF077760 Oryza sat
21	259	28.2	768	8	AY436722	AY436722 Drimys wi
22	256.2	27.9	851	8	AY436723	AY436723 Drimys wi
23	255.4	27.9	810	8	AY436725	AY436725 Drimys wi
24	254.4	27.7	1008	8	AF052874	AF052874 Papaver n
25	254.2	27.7	1166	8	AY541065	AY541065 Hordeum v
26	253	27.6	809	8	AY436724	AY436724 Drimys wi
27	253	27.6	828	8	ACA419959	ACA419959 Asarum ca
28	251	27.4	959	8	AB007506	AB007506 Trillium
29	247.4	27.0	834	8	ACA419955	ACA419955 Asarum ca
30	245.8	26.8	852	8	AY436715	AY436715 Saruma he
31	239.4	26.1	906	8	GHY9724	AJ009724 Gerbera h
32	239.4	26.1	958	8	AF627631	AF627631 Akebia tr
33	238.6	26.0	643	8	TAB577377	AJ577377 Trillium
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35	238.4	26.0	935	8	AY436736	AY436736 Lindera e
36	236	25.7	1257	6	AX478035	AX478035 Sequence
37	235	25.6	1004	8	AF181479	AF181479 Zea mays
38	233.4	25.5	810	8	AF230697	AF230697 Asarum eu
39	231.4	25.2	603	8	AY337748	AY337748 Perssea am
40	229.8	25.1	763	8	AY162861	AY162861 Platanus
41	228	24.9	946	6	AR372458	AR372458 Sequence
42	227.2	24.8	681	6	AR372459	AR372459 Sequence
43	226.8	24.7	755	8	AF230699	AF230699 Calycanth
44	226.8	24.7	767	8	AF130868	AF130868 Sanguinar
45	225.4	24.6	810	8	AY436709	AY436709 Meliosma

ALIGNMENTS

RESULT 1	AY378149	910 bp	mRNA	linear	PLN 09-AUG-2004
LOCUS	AY378149	Phalaenopsis equestris MADS box transcription factor (MADS2) mRNA,			
DEFINITION	complete cds.				
ACCESSION	AY378149				
VERSION	AY378149.1	GI:36680584			
KEYWORDS					
SOURCE					
ORGANISM	Phalaenopsis equestris				
	Phalaenopsis equestris				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;				
	Epidendroideae; higher Epidendroideae; Vandeeae; Aeridiinae;				
	Phalaenopsis.				
REFERENCE	1 (bases 1 to 910)				
AUTHORS	Tsai,W.C., Kuoh,C.S., Chuang,M.H., Chen,W.H. and Chen,H.H.				
TITLE	Four DEF-like MADS Box Genes Displayed Distinct Floral				
	Morphogenetic Roles in Phalaenopsis Orchid				
	Plant Cell Physiol. 45 (7), 831-844 (2004)				
JOURNAL	15295066				
PUBMED	2 (bases 1 to 910)				
REFERENCE	Tsai,W.C., Chen,W.H. and Chen,H.H.				
AUTHORS	Direct Submission				
TITLE	Submitted (02-SEP-2003) Department of Biology, National Cheng Kung				
JOURNAL	University, 1 University Rd., Tainan, Taiwan 701, Republic of China				
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Qy      483 GCATTAAGATATCATGTATGTGCGCACACAACTGACACTTACAGAAAAAGCTTTAAAG 542
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Qy      543 CACAAGGAAACTTACCGGCTCTAATATACATGAACTGATATA---TGAAGAGAGAAATCC 599
Db      722 CACAGACAAATATACAGAGCCCTTAACGCTAATCTGACAGAGCTGACAGAAAGATCA 781
Qy      600 GAATCAGGTTTTATGTAGAAAAACAGATAGAAATTTATGAATTCGATTCGAATGCT 659
Db      782 ACCGTCAGTTTTCTGTAAGAGATCTAAGCTGATATGACAGCTCAATCTCAATGGC 841
Qy      660 GAATGAGTCTCTCAGA 676
Db      842 AATCGGCTGCACCGA 858

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RESULT 3

AY196350 942 bp mRNA linear PLN 02-MAR-2003
LOCUS Oncidium cv. 'Gower Ramsey' MADS box protein (MADS3) mRNA, complete cds.

ACCESSION AY196350
VERSION AY196350.1 GI:28630894

KEYWORDS
SOURCE
ORGANISM

Oncidium cv. 'Gower Ramsey',
Oncidium cv. 'Gower Ramsey',
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Maxillarieae; Oncidiinae;
Oncidium.

REFERENCE 1 (bases 1 to 942)
AUTHORS Hsu, H.-F. and Yang, C.-H.

TITLE An Orchid (Oncidium Gower Ramsey) AP3-like MADS Gene Regulates Floral Formation and Initiation
JOURNAL Plant Cell Physiol. 43 (10), 1198-1209 (2002)
MEDLINE 22294943
PUBMED 12407200

REFERENCE 2 (bases 1 to 942)

AUTHORS Hsu, H.-F. and Yang, C.-H.
TITLE Direct Submision

Submitted (14-DEC-2002) Graduate Institute of Biotechnology,
National Chung-Hsing University, 250 Kuo-Kuang Rd., Taichung,
Taiwan 40227, Republic of China
Location/Qualifiers

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Query Match 37.0%; Score 339.2; DB 8; Length 942;
Best Local Similarity 74.0%; Pred. No. 9.3e-68;
Matches 444; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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Db      117 AGCAATGGGAGGAGAAAGATAGATTAAGATTAAGAAATTCACAAAGCAGCAAGT 176
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Qy      432 GCAACTGCGGCTTCTGAGCAAACTTTGGAAGTCTCTTAAGATTGTTAGCATAGAAA 491
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Qy      552 AACTTACCGGCTCTAATATCACTGA---GGAATGAAGAGAGAAATCCGAATCAAGG 608
Db      597 AATGTACCAAGCCCTTATGAATGAGCTGCAGAGGTTGATGAATGAATCAACAGCGCAG 656
Qy      609 TTTTAAATGTAGAAAACCAAGTAGAATTTATGAAAATTCGATTCGATGCTGAATGAGTG 668
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RESULT 4

AB094964 952 bp mRNA linear PLN 29-APR-2003
LOCUS Asparagus officinalis AODEF mRNA for MADS-box transcription factor, complete cds.

ACCESSION AB094964
VERSION AB094964.1 GI:30172218

KEYWORDS
SOURCE
ORGANISM

Asparagus officinalis (garden asparagus)
Asparagus officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Asparagus.

REFERENCE 1
AUTHORS Park, J., Ishikawa, Y., Yoshida, R., Kanno, A. and Kameya, T.
TITLE Expression of AODEF, a B-functional MADS-box gene, in stemens and inner tepals of dioecious species Asparagus officinalis L.
JOURNAL Plant Mol. Biol. (2002) In press

REFERENCE 2 (bases 1 to 952)
AUTHORS Kanno, A.
TITLE Direct Submision

Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi
980-8577, Japan (E-mail: kanno@ige.tohoku.ac.jp, Tel: 81-22-217-5725,
Fax: 81-22-217-5725)
Location/Qualifiers

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 QY 554 CTTCACCGCGCTTAAATCATGAACTGATATGAAAAGAGAAATCCGAACTTACGTTTAA 613
 DB 686 CACACCGGAACTTAAATCATGAACTGATATGAAAAGAGAAATCCGAACTTACGTTTAA 745
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 DB 800 ACATGATGCTTCCCGG---GTGCAACCCCAACCAAAATCTTCAAGAGAACGGATATA 856
 QY 734 AATCAATGATCTTACGCTTGCATTAAT 760
 DB 857 GCTCTCAGCATCTTCGCTCGCTTGAT 883

RESULT 6
 LOCUS AY378150 980 bp mRNA linear PLN 09-AUG-2004
 DEFINITION Phalaenopsis equestris MADS box transcription factor (MADS3) mRNA,
 complete cds.

ACCESSION AY378150
 VERSION AY378150.1 GI:38680586
 KEYWORDS Phalaenopsis equestris
 ORGANISM Phalaenopsis equestris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
 Epidendroideae; higher Epidendroideae; Vandaeae; Aeridinae;
 Phalaenopsis.

REFERENCE 1 (bases 1 to 980)
 Tsai, W.C., Kuo, C.S., Chuang, M.H., Chen, W.H. and Chen, H.H.
 Four DRE-Like MADS Box Genes Displayed Distinct Floral
 Morphogenetic Roles in Phalaenopsis Orchid
 Plant Cell Physiol. 45 (7), 831-844 (2004)

JOURNAL PUBMED 15295066
 REFERENCE 2 (bases 1 to 980)
 Tsai, W.C., Chen, W.H. and Chen, H.H.
 Direct Submision
 Submitted (02-SEP-2003) Department of Biology, National Cheng Kung
 University, 1 University Rd., Tainan, Taiwan 701, Republic of China
 Location/Qualifiers

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 Query Match 34.5%; Score 316.8; DB 8; Length 980;
 Best Local Similarity 65.3%; Pred. No. 1,4e-62;
 Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

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RESULT 7
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 DEFINITION Lilium regale LRDF mRNA for MADS-box transcription factor,
 complete cds.
 ACCESSION AB071378
 VERSION AB071378
 KEYWORDS Lilium regale
 ORGANISM Lilium regale
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;

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Db		666	GATGGTTATGAGCTCCCATGATCTCCGACTGGCTTGA	702
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RESULT_9		AF209729	833 bp mRNA linear PIN 01-DEC-2000	
LOCUS		AF209729	Hemerocallis hybrid cultivar putative MADS box transcription factor	
DEFINITION		(MADS1) mRNA, complete cds.		
ACCESSION		AF209729		
VERSION		AF209729.1	GI:11494136	
KEYWORDS				
SOURCE				
ORGANISM			Hemerocallis hybrid cultivar (daylily)	
			Hemerocallis hybrid cultivar Euryotia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Asparagales; Hemerocallidaceae; Hemerocallis.	
REFERENCE			1 (bases 1 to 833)	
AUTHORS			Lange,N.E.	
TITLE			Molecular changes during the expansion and senescence of ethylene-insensitive daylily flowers Thesis (1999) University of California, Davis	
JOURNAL			2 (bases 1 to 833)	
REFERENCE			Lange,N.E., Valpuesta,V., Napoli,C.A., Labavitch,J.M. and Reid,M.S	
AUTHORS			Direct Submission	
JOURNAL			Submitted (30-NOV-1999) Environmental Horticulture, University of California, Davis, CA 95616-8587, USA	
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ORIGIN	Query Match	32.2%	Score 295.6	DB 8	Length 833
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QY	256 TCTACTGATATTAAGGGATATATGAGAGGTACCAAGGTTGACTGGAATGATCTATG	315			
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QY	316 AATGCTCAGTATGAGAGATGACAGAAATACGCTGAAGCATCTGAATGAGATTAAACCAAAAC	375			
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QY	376 CTGAGGAAGAGATTAAGGAGGAGGAGGAGGAAATTGAGGCGATGCACTAAAGCA	435			
DB	301 TTGGCGCAAGAAATTAAGCAAGAGATGAGAGGAACCTTGATGCGATGATTTCAAGAA	360			
QY	436 CTGGCGGCTCTTGAGCAAACTTTGGAAGAGTCTCTTAAGATTGTTAGCATAGAAAGTAT	495			
DB	361 CTGGCGGCTCTTGAGCAAAATCTGGATGAGACTTTGAAGAGTGTTCGGCGTGAAGAAATAT	420			
QY	496 CATGTGATCGGCACACAACTGACACTTACCAAGAAAAGCTTAAGACCAAGGAAACT	555			
DB	421 CATGTGATTCACCTCAGACTGATACCTACCAAGAAAAGGAGGAATTCCTCAAGAAACA	480			
QY	556 TACCGCGCTCAATCAATCAAGACTGATATGAAAGAGGAATCCGAATCAAGCTTATAT	615			
DB	481 CACAAAGCTTTGCTGACGAACTTGATGACGCACTGTA-----TGATAT	525			
QY	616 GTAGAAAACAGATAGATTAATTAAGAAATTCGATTCGAATGATGAGTGTCTCAG	675			
DB	526 GCGATAGAGACCAAGCAACTATGATATGTTCACTTGCTGTCATGTGGGTCCAAAC	585			
QY	676 ATGTTTCTTTAAGGTTGTCATCCGATACGCCCAATCTGCTTGTTAGTTATGAA	735			
DB	586 ATGATGCTTACCG---AGTTCAACCAAGCCAGCAAACTCATGTGCATGACGTATGGG	642			
QY	736 TCACATGATCTTACGCTTGCATATG	761			
DB	643 CCACATGATCTTGGCTTGACATGATG	668			

RESULT 10	AF230706	938 bp	mRNA	linear	PLN 02-JUN-2000
LOCUS	AF230706				
DEFINITION	Tacca chandleri MADS box transcription factor AP3 mRNA, partial				

Db	241	AATTCCTATTACGAGAAAATGCAAGCTCATTGAAACAACTCAAGAGATTAATTAACAAT	300
Qy	376	CTAGGAAGAAGATTAGAGGAGGAAGGGGAGAAATTGGAGGGCATGAGACATTAAGCA	435
Db	301	CTCCGAGGGAGATCAAGCAAAAGATTGTGTAAAGTCTGAAAGATCTAGAAATCGAGAG	360
Qy	436	CTGGCGGCTTTGAGCAAACTTTGGAAAGTCTCTTAAGATTGTTAGGCATAGAAATAT	495
Db	361	CTGGCGGCTTTGAGCAAAATCTGAGCGATTTCTATCAATTTGTTCTGAGAGAAAGTAT	420
Qy	496	CATGTGATTCGCAACAACCTGACACTTAACAAGAAAAAGCTTAAAGACAAAGGAAACT	555
Db	421	CATGTGATTCGCACTCAACTGAGACTTACAAAGAAAAGCTGAGAACTTGGACAGAACCA	480
Qy	556	TACCGCGCTCTAATATACATGAACGTGATATGAAAGAGAGAAATCCGAACTACGGTTTAAT	615
Db	481	CATCAGCTTTAGTAGCGCTGATTGGAGAGACAAGCTGAGAAATGGGGCATATGGGTT---G	537
Qy	616	GTAGAAAACCAAGATAGAAATTATAGAAAATTCGATTCCAAATGAGTGAATGAGTGTCTCA	674
Db	538	GTGATGATGTGTGGCCAGACTATGAACTCTGACTCTGTTTGGCCAAATGTGTGTCTCTA	596

[illegible]

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES source	
1 (bases 1 to 651) Kim, S., Soltau, D.E. and Soltau, P.S. Pre-angiosperm duplication of floral genes and regulatory tinkering at the base of flowering plants Unpublished	
2 (bases 1 to 651) Kim, S., Soltau, D.E. and Soltau, P.S. Direct Submission Submitted (09-JUN-2003) Dept. of Botany, University of Florida, P.O. Box 118526, Gainesville, FL 32611, USA location/Qualifiers 1. 651	

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ORIGIN

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Query Match	31.1%	Score	285.4	DB	8	Length	651
Best Local Similarity	68.4%	Pred. No.	2.5e-55				
Matches	410	Conservative	0	Mismatches	186	Indels	3
						Gaps	1

Qy	76	ATGGGAGAGGGGAGATGAGATATAAAAGATAGAGATCCGACAAACAGGCAAGTATCA	135
Db	1	ATGGGAGAGAGAAAGATCGAGATATAAAAGATAGAGATTCACATACAGCAAGTGA	60
Qy	136	TATCTTAAGAGAGAGTGGGATCTGTAAGAAAGCCAGAGAGCTCACTGTTCTCTGATAT	195
Db	61	TACTCTGAAGAGAGAGTGGGATTTATGTAAGAAAGCTTAAGAGACTTACTGTTCTCTGAT	120

Qy	196	GCACAGCTCTCTCATCAAGTTCTCAAGACAGGAAGTTGGCTGATTCTCGACGCC	255
Db	121	GCAGAGTTTCTCTATTATGTTCTCCAAATACGGCAAGTTCTCGAATCTGAGCCCT	180
Qy	256	TCCTACTGATTTTAAAGGGATATATAGAGGTACAGTTTGACTGGAATGATCTATGG	315
Db	181	TTCTACACGACTAAGAAAGATTTTGCATGCTTACCGAAGTTTACACCAACTTGGG	240
Qy	316	AATGCTCAGATATAGAGGATGCAAGATACGCTGAGCATCTGAATGAATTAACCAAC	375
Db	241	AATTCCTATTACGGAATAATGCAAGCTCATTTGAACCAACTCAAAAGAGATTAATAAAT	300
Qy	376	CTGAGGAAGAGATTAGAGAGGAAGGGGAGGAATTGAGGCGCATGSCATTAACCA	435
Db	301	CTCCGAGGAGATCAGGCAAAAGGATTTGGTAAGATCTGGAAGATTCTAGAAATGAGAG	360
Qy	436	CTGGCGCGTCTTGAAGCAATTTGGAAAGATCTCTTGAATTGTTAGCATAGAAAGTAT	495
Db	361	CTGGCGCGTCTTGAAGCAAAATCTGGAGGATTTCTATCAAAATTTGTTCTGAGAGAAATAT	420
Qy	496	CATGTATGCGCACACAACTGACACTTACAAAGAAAAGCTTAAAGCACACAGGAACT	555
Db	421	CATGTATGCGCACACTCAACTGAGACTTTCAAGAAAAGCTGAGAACTTGACAGAAACA	480
Qy	556	TACCGCGCTCTAATATACATGAATCTGATATGAAGAAGAGAAATCCGAATCAGGTTTAAAT	615
Db	481	CATCAGCTTTAGTACGTGCAATGGAAAGCACAGCTGATGAAATGGGGATATGGGTT---G	537
Qy	616	GTAAAGAAACAGAGTAGAATTTATGAAGAAATTCGATTCGAATGGTAATGATGTCCTCA	674
Db	538	GTGATATATGATGGGCCAGACTATGAATCTGCACTTCTTGGCCAAATGATGTCCTCA	596

RESULT 13	
LOCUS	AB050649
DEFINITION	AB050649 852 bp mRNA linear PLN 31-OCT-2001
ACCESSION	Magnolia praecoccissima mRNA for putative MADS-domain transcription factor MpMADS7, complete cds.
VERSION	AB050649
KEYWORDS	AB050649.1 GI:16549069
SOURCE	Magnolia praecoccissima
ORGANISM	Magnolia praecoccissima

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Ito, M., Shiohara, S., Tanabe, Y. and Hasebe, M.
Organ identifications in Magnolian flower
Unpublished
2 (bases 1 to 852)
Ito, M., Shiohara, S. and Hasebe, M.
Direct Submission
Submitted (31-OCT-2000) Motomi Ito, University of Tokyo, Department
of Systems Sciences, Graduate School of Arts and Sciences; 3-8-1
Komaba, Meguro-ku, Tokyo 153-8902, Japan
(E-mail: cmic@mail.ecc.u-tokyo.ac.jp, Tel: 81-3-5454-6638,
Fax: 81-3-5454-6638)

FEATURES
SOURCE

Location/Qualifiers
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ORIGIN

Query Match 31.1%; Score 284.8; DB 8; Length 852;
Best Local Similarity 70.7%; Pred. No. 3.4e-55;
Matches 379; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

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QY 196 GGTCAAGTCTCTCTATCATATGTTCTCAAGACAGAGAAATGGCTGATTACTGACGCC 255
DB 121 GCTCAAGTCTCTCTATCATATGTTCTCAAGACAGAGAAATGGCTGATTACTGACGCC 255
QY 256 TCTACTGATATTAAAGGGGATATATAGAGGTAACGAGTGTGACTGGAATGATCTATGG 315
DB 181 TCTACACACGAGAGATATTTTTCGATCGTTACCGAGAGCTTCGGGCACTCAGCTTATGG 240
QY 316 AATGCTAGTATGAGAGATGACAGAAATCCGTAGACATCTGAATGATTAACCAAAAC 375
DB 241 AACTCTACTACGAGAGATGACAGAAATCCGTAGACATCTGAATGATTAACCAAAAC 375
QY 376 CTGAGAGAGAGATGAG 435
DB 301 CTCGGAGAGAGATGAG 360
QY 436 CTGCGGGGCTTTAGCAAACTTTGGAAGAGTCTCTTAAGATTTGTAAGCATTAAGATAT 495
DB 361 CTGCGGGGCTTTAGCAAACTTTGGAAGAGTCTCTTAAGATTTGTAAGCATTAAGATAT 495
QY 496 CATGTATCGCCACCAACCTGACCTTAACAAGAAAGCTTAAAGACCAAGGAAACT 555
DB 421 CATGTATCGCCACCAACCTGACCTTAACAAGAAAGCTTAAAGACCAAGGAAACT 555
QY 556 TACCGGCTCTTAATACATGAATGTGATATGAAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 481 CACGCAAAATTAATTCGTCATTTGGAGGTCAAGCTGAGAAACGGGGCTTACGGCTT 536

RESULT 14

AB094965 1002 bp mRNA linear PIN 31-OCT-2003
LOCUS Tulipa gesneriana TGDEFA mRNA for MADS-box transcription factor.
ACCESSION AB094965
VERSION AB094965.1 GI:30172220
KEYWORDS
SOURCE
ORGANISM

REFERENCE

AUTHORS Kanno,A., Saeki,H., Kameya,T., Saedler,H. and Theissen,G.
TITLE heterotopic expression of class B floral homeotic genes supports a
JOURNAL modified ABC model for tulip (Tulipa gesneriana)
MEDLINE Plant Mol. Biol. 52 (4), 831-841 (2003)
PUBMED 13677470
2 (bases 1 to 1002)
REFERENCE Kanno,A.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
School of Life Sciences, Aoba-ku, Katahira 2-1-1, Sendai, Miyagi

FEATURES
source
location/Qualifiers
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DB 612 GGTCTTAATGAG 611
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ORIGIN

Query Match 30.8%; Score 282.2; DB 8; Length 1002;
Best Local Similarity 65.6%; Pred. No. 1.3e-54;
Matches 464; Conservative 0; Mismatches 228; Indels 15; Gaps 3;

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QY 316 AATGCTAGTATGAGAGATGACAGAAATCCGTAGACATCTGAATGATTAACCAAAAC 375
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DB 612 GGTCTTAATGAG 611
QY 667 TGTCTCAGATGTTTCTTTAGAGTGTTCATCCGAATCAACCCCAATCTGTTGTTA 726
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LOCUS     Tulipa gesneriana TGDBFB mRNA for MADS-box transcription factor,
AB094966 complete cds.
VERSION   AB094966.1 GI:30172222
KEYWORDS
SOURCE    Tulipa gesneriana
ORGANISM  Tulipa gesneriana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
           Tulipa.
REFERENCE
AUTHORS   Kanno,A., Saeki,H., Kameya,T., Saedler,H. and Theissen,G.
TITLE      Heterotopic expression of class B floral homeotic genes supports a
JOURNAL    modified ABC model for tulip (Tulipa gesneriana)
MEDLINE    Plant Mol. Biol. 52 (4), 831-841 (2003)
2286392
PUBMED     13677470
REFERENCE   2 (bases 1 to 1016)
AUTHORS    Kanno,A.
TITLE      Direct Submision
JOURNAL     Submitted (28-OCT-2002) Akira Kanno, Tohoku University, Graduate
980-8577, Japan (E-mail:kanno@ge.tohoku.ac.jp, Tel:81-22-217-5725,
Fax:81-22-217-5725)
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gene
cds

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ORIGIN

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Query Match      29.0%; Score 265.8; DB 8; Length 1016;
Best Local Similarity 64.0%; Pred. No. 8.1e-51;
Matches 437; Conservative 0; Mismatches 237; Indels 9; Gaps 2;

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 Job time : 3963 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 17:04:00 ; Search time 415 Seconds
(without alignments)
11599.323 Million cell updates/sec

Title: US-10-690-246-1

Perfect score: 917

Sequence: 1 acgcggagatagtagaggaag.....ttttcttcttctttttcgg 917

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
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- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	245.2	26.7	637	10	ADKS9650	Adk59650 Plant DNA
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3	234.8	25.6	681	12	ADJ44530	Adj44530 Plant cDN
4	228	24.9	946	4	AAE85392	AAE85392 Nucleoid
5	228	24.9	946	6	ABK8485	ABK8485 Poplar pr
6	228	24.9	946	6	ACA62518	ACA62518 Poplar ho
7	227.2	24.8	681	4	AAE85393	AAE85393 Nucleoid
8	223.2	24.3	924	3	AAZ57943	AAZ57943 Poplar fl
9	216.6	23.6	989	3	AAE5879	AAE5879 Eucalyptu
10	214.4	23.4	954	3	AAE51525	AAE51525 Arabidops
11	213.8	23.3	1170	3	AAE51790	AAE51790 Arabidops
12	213.2	23.2	988	12	ADO61550	ADO61550 Transcrip
13	211.6	23.1	959	3	AAE40831	AAE40831 Arabidops
14	209.8	22.9	664	10	ADKS6100	Adk6100 Plant DNA
15	209.8	22.9	665	10	ADKS9635	Adk9635 Plant DNA
16	207.2	22.6	926	6	AAD42259	Aad42259 Soybean A
17	203.4	22.2	630	10	ADKS9791	Adk9791 Plant DNA
18	202.4	22.1	954	3	AAE40685	AAE40685 Arabidops
19	201.2	21.9	498	12	ADP95468	Adp95468 Cotton ex
20	200.8	21.9	882	2	AAO51189	AAO51189 Homeotic
21	194.8	21.2	982	4	AAO50104	AAO50104 Gramny Sm

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24	168	18.3	401	12	ADQ03167	Adq03167 Arabidops
25	161	17.6	868	4	AAO0103	AAO0103 Gramny Sm
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27	159.2	17.4	386	3	AAE57268	AAE57268 Eucalyptu
28	155.2	16.9	360	12	ADQ03169	Adq03169 Arabidops
29	154.4	16.8	947	3	AAE39436	AAE39436 Arabidops
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31	153.8	16.8	914	12	ADQ01552	Adq01552 Transcrip
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34	148.6	16.2	474	12	ADP95656	Adp95656 Cotton ex
35	145.6	15.9	742	10	ADKS6091	Adk6091 Plant DNA
36	144.2	15.7	632	10	ADKS5993	Adk5993 Plant DNA
37	143.4	15.6	409	3	AAE56790	AAE56790 Eucalyptu
38	142.4	15.5	909	3	AAE35208	AAE35208 Arabidops
39	132.6	14.5	310	12	ADP94956	Adp94956 Cotton ex
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41	129.8	14.2	340	12	ADP91369	Adp91369 Cotton ex
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ALIGNMENTS

RESULT 1	ADKS9650	ADKS9650	standard; DNA; 637 BP.
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AC	ADKS9650:		
DT	06-MAY-2004	(first entry)	
XX	Plant DNA sequence which confers altered metabolic characteristic #7033.		
XX	altered metabolic characteristic; plant; acid metabolism;		
KW	alcohol metabolism; fatty acid metabolism;		
KW	branched fatty acid metabolism; alkaloid metabolism;		
KW	amino acid metabolism; ester metabolism; glyceride metabolism;		
KW	phenolic metabolism; carbohydrate metabolism; steroid metabolism;		
KW	terpene metabolism; isoprenoid metabolism; alkene metabolism;		
KW	alkyne metabolism; hydrocarbon metabolism; ketone metabolism;		
KW	quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.		
XX	Unidentified.		
OS	Unidentified.		
XX	WO2003020936-A1.		
XX	13-MAR-2003.		
PD	30-AUG-2002; 2002WO-US027884.		
PF	30-AUG-2001; 2001US-0316471P.		
XX	31-AUG-2001; 2001US-0316471P.		
XX	(DOWC) DOW CHEM CO.		
PA	(DOWC) DOW AGROSCIENCES LLC.		
XX	Weglarz T, Gachotte D, Blakeslee B, McCreary DA, Pell RJ,		
PI	Oriedo JVB, Crossley R, Reddy AS, Shukla V, Larrinua I, Miller BA;		
XX	WPI; 2003-313091/30.		
DR	Novel genes that confer altered metabolic characteristics in Nicotiana		
PT	benchamiana plants, useful for altering the levels of metabolites e.g.		
PT	acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.		
XX	Claim 1; SEQ ID NO 7033; 2576pp; English.		
PS	The invention comprises DNA sequences which confer an altered metabolic		
XX			
CC			

430 GCIGCGCCCTCGAGCAAAACGTGACGGGCTCTCAAGAGGTTCCCATAGGAAGTA 549

[illegible]

KW LFY; FLORICAUDIA; FLO; DEFICIENS; DEF; AGAMOUS; AG; transgenic plant;
 KW fertility; sterility; ss.

OS Populus balsamifera.

FT Key Location/Qualifiers
 CDS 1..684
 /*tag= a
 /product= "PTD"

CA2319853-A1.

01-APR-2001.

02-OCT-2000; 2000CA-02319853.

01-OCT-1999; 99US-00410464.

(UYOR-) UNIV OREGON HEALTH SCI.

Rotman WH, Straus SH, Brunner AM, Sheppard LA;
 WPI; 2001-336098/36.
 P-PSDB; AAB68435.

Novel isolated polynucleotide derived from Populus species, useful for
 producing transgenic plants having modified fertility characteristic,
 particularly sterility.

Claim 25; Page 41-42; 69pp; English.

The present sequence encodes a floral homeotic protein, designated PTD.
 It is derived from Populus balsamifera subsp. trichocarpa. The
 CC specification also describes PTLF, PTA-1 and PTA-2 proteins. The
 CC homeotic proteins are expressed in floral tissues. PTLF is a homologue of
 CC LEAFY (LFY) and FLORICAUDA (FLO), and is expressed in immature
 CC inflorescences on which floral primordia are developing. PTD is a
 CC homologue of DEFICIENS (DEF), and is strongly expressed in stamen
 CC primordia from the onset of organogenesis. PTA-1 and PTA-2 are
 CC homologues of AGAMOUS (AG). The floral homeotic proteins and
 CC polynucleotides are useful for producing transgenic plants having
 modified fertility characteristics, particularly sterility

Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 4; Length 946;
 Best Local Similarity 58.3%; Pred. No. 2.1e-48;
 Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGAGATGAGATTAAGATAGAGATCGAGCAAGCAAGTTACA 135
 DB 1 ATGGGTGTGGAAGATTGAATCAAGATCGAAGATCCCAAGAGGCAAGTCAAC 60
 QY 136 TATTCTAAGAGAGAGTTGGATCTGAAGAGCCCAAGAGCTCTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAAATGTTATTTTCAGAAAGCCCAAGAACTCACTGACTTGTGAT 120
 QY 196 GCTCAGGTCTCTCATCATGTTTCTCAACACAGAAAGTTGGCTGATTACGACCCC 255
 DB 121 GCTAAGGTCTCTTATCATGTTCTCAACACTCACTCAAGTCACTGATGCTGAT 180
 QY 256 TCTAAGTATTAAGGGATATATGAGAGTACAGAGTTGCTGATGAGATGATATG 315
 DB 181 TCCACATCGACAAAGATCTACGATCAATATCAAGACGCTTTAGGATATGATCTG 240
 QY 316 AATGCTCATATGAGAGATGAGATACGCTGAAGCATCTGAATGATTAACCAAC 375
 DB 241 GGCATCATATACGAGAAATGCAAGAGCCTTGAAGAGCTGATGATTAATCATAG 300
 QY 376 CTGAGAGAGAGATTAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 435
 DB 301 CTGAGCAAGAAATCAGCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 360

QY 436 CTGCGCGGTCTTGAAGCAACTTTGAAGAGTCTCTTAAGTTAGCATAGAAATAT 495
 DB 361 CTGCGCGGTCTTGAAGCAACTTTGAAGAGTCTCTTAAGTTAGCATAGAAATAT 420
 QY 496 CATGATGATGCGCAACAACTGACATCTTCAAGAAAAAGTTAAAGCAAGGAAACT 555
 DB 421 CATGATGATGCGCAACAACTGACATCTTCAAGAAAAAGTTAAAGCAAGGAAACT 480
 QY 556 TACCGCGGTCTTGAAGCAACTTTGAAGAGTCTCTTAAGTTAGCATAGAAATAT 615
 DB 481 CATGAAACCTCTTGAAGCAACTTTGAAGAGTCTCTTAAGTTAGCATAGAAATAT 540
 QY 616 GTAGAAAACAGAGTGAATTTATGAATTTGATTCAGTGAATGAGTCTCTAG 675
 DB 541 GACATGAGTCTGTTGATGATGCACTTGAAGAGGAGGAGGAGGAGGAGGAGGAG 600
 QY 676 ATGTTTCTTGAAGGAGTGTTCAGCAATTCAGCCCAATCTGCTTGAAGTTAG 735
 DB 601 CATCAGGAGCAACACCAACCACTTCCTTAATCTTACCTTGAAGAGATTTGA 759
 QY 736 TCACATGATTTAGCTTGCATTA 759
 DB 661 GCCATGAACCTTGCCTTCTTGA 684

RESULT 5

ABK88485
 ID ABK88485 standard; cDNA; 946 BP.

AC ABK88485;

DT 29-AUG-2003 (revised)
 DT 07-OCT-2002 (first entry)

DE Poplar protein transduction domain, PTD, cDNA.

KW Poplar; ss; gene; plant; DEFICIENS; transgenic; promoter;
 KW protein transduction domain; floral homeotic gene;
 KW floral-specific expression; cytoloxin; fertility; sterility; PTLF;
 KW PTA-1; PTA-2.

OS Populus balsamifera; subsp. trichocarpa.

FT Key Location/Qualifiers
 CDS 1..684
 /*tag= a
 /product= "PTD"

US6395892-B1.

28-MAY-2002.

01-OCT-1999; 99US-00410464.

06-APR-1998; 98US-0080851P.
 06-APR-1999; 99US-00287700.

(UYOR-) UNIV OREGON HEALTH SCI.

Straus SH, Rotman W, Brunner A, Sheppard L;
 WPI; 2002-572853/61.
 P-PSDB; AEG30865.

New protein transduction domain promoter nucleic acid molecule useful for
 producing transgenic plants having modified fertility characteristics,
 particularly sterility.

Example 1; Col 35-38; 46pp; English.

The invention relates to an isolated nucleic acid molecule especially a
 CC protein transduction domain (PTD) promoter; (i) that hybridizes under
 CC wash conditions of 0.2 x SSC (sodium chloride), 0.1 %SDS (sodium

CC dodecyl sulphate) at 65 plusoc to nucleotides or (1) comprising 35
 CC consecutive nucleotides of the PTD gene. PTD is a floral homeotic gene
 CC and is the homologue of DEFICIENS. Also includes a recombinant
 CC nucleic acid comprising the PTD promoter, a cell transformed with the
 CC recombinant nucleic acid and a transgenic plant comprising the
 CC transformed cell. The PTD promoter is useful to obtain floral-specific
 CC expression of genes such as cytotoxins, that are employed in genetic
 CC ablation strategies to produce trees having modified fertility
 CC characteristics, including sterility. Genetic constructs comprising
 CC antisense versions or dominant negative mutants of PTD are useful in
 CC producing genetically engineered Poplars and other trees, and for sense
 CC suppression. Also disclosed are 3 other homeotic genes PTF, PTA-1 and
 CC PTA-2 (none are defined). The present sequence is the PTD cDNA. (Updated
 CC on 29-AUG-2003 to standardize OS field)

XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 6; Length 946;

Best Local Similarity 58.3%; Pred. No. 2,1e-48; Mismatches 285; Indels 0; Gaps 0;

Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGAGATAGATATAAAGATAGATCCGACGAAAGGCAAGTTACA 135
 DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAAAGATGAAAACCCCAAAACAGGCAAGTCACC 60
 QY 136 TATTTTAAGAGAGAGTTGGGATCTGAAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAAATGATGATTTTTCAGAAAGCCCAAGAACTCACTGATCTTTGAT 120
 QY 196 GCTCAGGTCCTCTCATCATGTTCTCAAGACAGAAAGTTGGCTGATTACTCAGACCCC 255
 DB 121 GCTAAGGTCCTCTTATCATGTTCTCCAACTCACTCAACTCAATGATGATTAAGCCCC 180
 QY 256 TCTACTGATATTAAGGGATATATGAGAGTACAGGTTGTGATCGAATGATCTATGG 315
 DB 181 TCCACATCGACAAAGAAATCTAGATCATATCAAGAGCTTTAGGCAATGATCTGTGG 240
 QY 316 AATGTCAGTATGAGAGATGACGAATPAGCTGAAGCATTTGAATGATTAACCAAAAC 375
 DB 241 GGCACCTCAATACAGAAATGCAAGAGCACTTGAAGAGCTGATGATATCAATCATTAAG 300
 QY 376 CTGAGAGAGAGATTGAG 435
 DB 301 CTGAGACAAAGAAATCAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 436 CTGCGGGCTCTTGAGCAAACTTTGAAAGATCTTTGAATTTGAGCATAGAAATAT 495
 DB 361 CTGCGGGCTCTTGAGCAAACTATGACTGAAGCTTTGATGTTGTTGGTGGCAGAGAGTAC 420
 QY 496 CATGTATGCGACACAACTGACACTTACAGAAAAAGCTTAAAGACACAGAGAACT 555
 DB 421 CATGTATCAAAAACAAACGAAACCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 QY 556 TACCGGCTCTTATACATGAACTGATATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 615
 DB 481 CATGAAACCTCTTATGATGATATGAAGCAAACTGAGAGATGACGATGTTAGTG 540
 QY 616 GTAGAAACAGAGATGAAATTTATGAAATTCGATTCGATGATGATGATGATGATGAT 675
 DB 541 GAAACAGAGAGCTCTGTTGCACTTGCAAAAGGGGCTTCAACTGATGATGATGATGAT 600
 QY 676 AGTTTCTCTTAAAGGTTGTTCAATCCGAAATCAAGCCCAATGCTGTTGTTAGTTTAA 735
 DB 601 CATCAGGGGACACACCAACCACTCTCTTATCTTCACTTGAAGATGATGATGATGAT 660
 QY 736 TCACATGATCTTAGCTTGATTA 759
 DB 661 GCCCATGAACCTGCTCTTGA 684

RESULT 6
 ACA62518
 ID ACA62518 standard; cDNA; 946 BP.

XX ACA62518;
 AC 18-AUG-2003 (first entry)
 DT 18-AUG-2003 (first entry)
 DE Poplar homeotic gene PTD, cDNA.
 XX Poplar, 88; gene; PTD; deficiens; homeotic gene; floral development;
 KW sterile tree; pulp; paper; plant.
 XX Populus balsamifera subsp. trichocarpa.
 OS Key Location/Qualifiers
 FH CDS 1..684
 FT /tag= a
 FT /product= "PTD"
 FT /note= "This CDS is specifically claimed in claim 1"
 PN US2003033628-A1.
 PD 13-FEB-2003.
 PD 21-MAR-2002; 2002US-00104580.
 PF 06-APR-1998; 98US-0080851P.
 PR 06-APR-1999; 99US-00287700.
 PR 01-OCT-1999; 99US-00410464.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 PA Strauss SH, Rottmann W, Brunner A, Sheppard L,
 PI WPI; 2003-466273/44.
 DR P-PSDB; ABUS1893.
 DR New floral homeotic nucleic acid molecules, useful for the manipulation
 PT of flowering in Poplar and other plant species, and for producing
 PT transgenic plants having modified fertility characteristics, particularly
 PT sterility.
 PS Claim 1; Page 20-21; 48pp; English.
 XX The invention relates to an isolated nucleic acid molecule comprising at
 CC least 15 consecutive nucleotides of the gene, cDNA or coding sequence of
 CC 4 homeotic genes from Poplar, PTF (LEAFY and FLORIDA homologue), PTD
 CC (DEFICIENS homologue), and PTA-1/PTA-2 (both homologues of AGAMOUS).
 CC Also included are a recombinant nucleic acid molecule comprising a
 CC promoter sequence operably linked to the nucleic acid molecule, a cell
 CC transformed with the nucleic acid molecule, a transgenic plant comprising
 CC the recombinant nucleic acid molecule and the purified proteins encoded
 CC by the nucleic acids. The nucleic acid molecules are useful for the
 CC manipulation of flowering in Poplar and other plant species, for
 CC producing transgenic plants having modified fertility characteristics
 CC (particularly sterility) and in the pulp and paper industries. The
 CC present sequence is the poplar PTD cDNA.

XX Sequence 946 BP; 331 A; 184 C; 201 G; 230 T; 0 U; 0 Other;

Query Match 24.9%; Score 228; DB 9; Length 946;

Best Local Similarity 58.3%; Pred. No. 2,1e-48; Mismatches 285; Indels 0; Gaps 0;

Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGAGATAGATATAAAGATAGATCCGACGAAAGGCAAGTTACA 135
 DB 1 ATGGGTCGTGGAAGATTGAAATCAAGAAAGATGAAAACCCCAAAACAGGCAAGTCACC 60
 QY 136 TATTTTAAGAGAGAGTTGGGATCTGAAAGAGCCCAAGAGCTCACTGTTCTGTGAT 195
 DB 61 TACTCGAAGAGAAATGATGATTTTTCAGAAAGCCCAAGAACTCACTGATCTTTGAT 120
 QY 196 GCTCAGGTCCTCTCATCATGTTCTCAAGACAGAAAGTTGGCTGATTACTCAGACCCC 255
 DB 121 GCTAAGGTCCTCTTATCATGTTCTCCAACTCACTCAACTCAATGATGATTAAGCCCC 180

RESULT 8
AAZ57943
ID AAZ57943 standard; cDNA, 924 BP.
XX
AC AAZ57943;
XX
DT 11-APR-2000 (first entry)
XX DE Poplar floral homeotic gene PTD cDNA.
XX
KW Poplari; PTD; floral homeotic gene; transgenic plant; sterility;
KM fertility; ss.
XX
OS Populus balsamifera subsp. trichocarpa.
XX
FH Location/Qualifiers
FT 1..684
FT CDS /tag= "a
FT /note= "the coding region is also specifically claimed in
FT Claim 1"
PN CA2227940-A1.
PD 06-OCT-1999.
PF 07-APR-1998; 98CA-02227940.
PR 06-APR-1998; 98US-00080851.
PA (UYOR-) UNIV OREGON HEALTH SCI.
PI Rottmann WH, Brunner AM, Sheppard LA, Straus SH,
PI MPI: 2000-106662/10.
DR P-PADB; AAY58654.
XX
XX Nucleic acid from Populus trichocarpa genes, useful for producing
PT transgenic plants, particularly trees, with modified fertility
PT characteristics such as sterility.
PS Claim 1; Page 46-47; 92ap; English.

The present sequence is that of cDNA encoding Populus balsamifera subsp. trichocarpa PTD protein (see AAY58654). The PTD gene (see AAZ57942) is a newly identified floral homeotic gene from this poplar species. It is a homologue of DBFICENS and is expressed strongly in stamen primordia from the onset of organogenesis, and is also expressed at low levels in carpel primordia. The invention provides nucleic acid sequences of these 4 Populus genes, the corresponding cDNA sequences (see AAZ57942-49) and deduced amino acid sequences (see AAY58454-57). It also provides methods of using the gene and cDNA sequences to produce genetically engineered Populus species and other trees having modified fertility characteristics, including sterility. Genetic constructs useful in producing genetically engineered Populus and other trees include antisense versions of PTD, dominant negative mutants, and constructs useful for sense suppression. Promoter sequences may be used to obtain floral specific expression of genes such as cytotoxins that may be used in genetic ablation strategies to produce trees having modified fertility characteristics, including sterility. Sterile trees allow increased wood yield and a reduction in the production of allergens such as pollen

Sequence 924 BP; 309 A; 185 C; 201 G; 229 T; 0 U; 0 Other;

Query Match 24.3%; Score 223.2; DB 3; Length 924;
Best Local Similarity 57.9%; Pred. No. 3.5e-47;
Matches 396; Conservative 0; Mismatches 286; Indels 0; Gaps 0

ATGGGAGAGGCGAAGATAGAGTAAAAAAGATAGAGAATCCGACGAAGCAGCAATTACA 135
|||||
1 ATGGGTGCTGGAAAAGATTGAATCATCAAGAAATCCGAAACCACCAAACAGCAATTCACC 60
|||||
136 TATTCTTAAGAGAGAGTTGGACTACTGAAGAACGCCAAGAGACTACTGTTCTCTTGAT 195

D	b		61	TACTCGAAGGAAGAATGGATTTTTCAAGAAAGCCAAAGACCTGTACTTGAT	120
O	y		196	GCTAGGTCTCTCATCATGTTCTCAAGACAAGAAAGTTGGCTGATTACGCACC	255
D	b		121	GCTAAGGTCTCTTATCATTTGTCGCCAACATAACAACTCATGTGATCATTAGCCC	180
O	y		256	TCATCTGATATTAAAGGGGATATTATGNAAGGTACAGTTGTGACTGGAAATGATCTTAG	315
D	b		181	TCGCATCTGACAAAAGAAATCTACGATCAATTCAGAACCTTTAGGCATGATCTGTGG	240
O	y		316	AATGCTCAGTATGAGAGGATGACAGAAATACGCTGAGCATGTAATGATTAACCAAAC	375
D	b		241	GGCACTCTAATACGAGAAATATCGAAGGACCTTTGAGAAAGCTGAATGATATCAATCA	300
O	y		376	CTGAGGAAGAGATTAGAGAGAGGAAGGGGAGGAATTTGAGGGCATGACATTAAGCAA	435
D	b		301	CTGAGACAAAGAAATCAGGACAGAGGAGAGAGAGGGCCTGTAATGATCTGAGCATTTGATCAT	360
O	y		436	CTGGCGCGTCTTGAAGCAAACTTTGGAAGAATCTCTTGAATTGTGAGCATTAAGAAATAT	495
D	b		361	CTGGCGCGTCTTGAAGCAAACTTGAAGCTTGAATGTGTGCGTGGCAGGAAGTAC	420
O	y		496	CATGTGATCGCACACAACTGACACTTACAGAAAAAGCTTAAAGACACAAGGAAACT	555
D	b		421	CATGTGATCAAAACACAAAACGAACCTTACAGGAGAGGTGAAGAAATTTAGAGAGAGA	480
O	y		556	TACCGCGCTTAAATPACATGAATCGATATGAAAAGAGAGAAATCGAACTACGGTTTTAAT	615
D	b		481	CATGGAACCTCTTGATGAAATATGAAGCAAACTAGAGGATGCACAGTATGGTTAGTG	540
O	y		616	GTAGAAAAACAGATAGAAATTTATGAAATTCGATTCCAATGGTGAATGATGTCCTCAG	675
D	b		541	GACAAATGAACCTGTGTTCGACTTGCAGAAATGGGGCTTCCAACCTTATGCAATTCGGCTG	600
O	y		676	ATGTTTTCTTTAGGGTGTTCATCCGATCCAGCCCAATCGCTTGTTAGGTTATGAA	735
D	b		601	CATACGGGGACACACACACACCATCTCCCTTAATCTTCACTTGGAGATGATTTTGA	660
O	y		736	TCAATGATCTTGAACCTTGCATTA	759
D	b		661	GCCCATGACACTGCGCTTCTTGA	684
RESULT 9					
AAC55879					
ID	AAC55879 standard; DNA; 989 BP.				
XX	AAC55879;				
AC	AAC55879;				
DE	25-JAN-2001 (first entry)				
OS	Eucalyptus grandis transcription factor DNA sequence #10.				
XX	Plant; transcription factor; gene expression; eucalyptus; pine; acacia;				
KM	poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;				
KW	basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;				
KV	homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;				
KM	type 2 Cys2His2; CCAT box element; MYB; ss.				
XX	Eucalyptus grandis.				
OS	WO200053724-A2.				
XX	14-SEP-2000.				
PF	09-MAR-2000; 200OMO-US006112.				
XX	11-MAR-1999; 99US-00266513.				
PR	18-AUG-1999; 99US-0149485P.				
XX	(GENE-) GENESIS RES & DEV CORP LTD.				
PA	(FLET-) FLETCHER CHALLENGE FORESTS LTD.				

The present invention relates to novel plant transcription factors from *Eucalyptus grandis* or *Pinus radiata*. The present sequence is the coding sequence for one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, bZIP family of G-box and homeotic/homeodomain/homeobox/MADS, homeodomain zipper, and ERBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and MYB

Yearly match	23.6%;	Score 216.6;	DB 3;	Length 989;
Best Local Similarity	64.4%;	Pred. No. 1.8e-45;		
Matches 324;	Conservative			

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RESULT 10
AAC51525
ID AAC51525 standard; DNA; 954 BP.
XX
AC AAC51525;
XX
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.

PR	8-JUN-1999	99US-0139873P
PR	21-JUN-1999	99US-0139887P
PR	23-JUN-1999	99US-0139899P
PR	23-JUN-1999	99US-0140353P
PR	23-JUN-1999	99US-0140354P
PR	24-JUN-1999	99US-0140655P
PR	28-JUN-1999	99US-0140823P
PR	29-JUN-1999	99US-0140991P
PR	30-JUN-1999	99US-0141287P
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PR	02-JUL-1999	99US-0142154P
PR	02-JUL-1999	99US-0142055P
PR	06-JUL-1999	99US-0142380P
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PR	12-JUL-1999	99US-0142977P
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PR	15-JUL-1999	99US-0143654P
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PR	13-AUG-1999	99US-0148368P
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PR	17-AUG-1999	99US-0149426P
PR	18-AUG-1999	99US-0149472P
PR	20-AUG-1999	99US-0149723P
PR	20-AUG-1999	99US-0149923P
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PR	23-AUG-1999	99US-0149930P
PR	25-AUG-1999	99US-0150566P
PR	26-AUG-1999	99US-0150884P
PR	27-AUG-1999	99US-0151065P

PR	27-AUG-1999;	99US-0151066P
PR	27-AUG-1999;	99US-0151080P
PR	30-AUG-1999;	99US-0151303P
PR	31-AUG-1999;	99US-0151438P
PR	01-SEP-1999;	99US-0151930P
PR	07-SEP-1999;	99US-0152363P
PR	10-SEP-1999;	99US-0153070P
PR	13-SEP-1999;	99US-0153768P
PR	15-SEP-1999;	99US-0154038P
PR	16-SEP-1999;	99US-0154039P
PR	20-SEP-1999;	99US-0154779P
PR	22-SEP-1999;	99US-0155139P
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PR	24-SEP-1999;	99US-0155659P
PR	28-SEP-1999;	99US-0156468P
PR	29-SEP-1999;	99US-0156566P
PR	04-OCT-1999;	99US-0157117P
PR	04-OCT-1999;	99US-0157753P
PR	05-OCT-1999;	99US-0157865P
PR	06-OCT-1999;	99US-0158032P
PR	07-OCT-1999;	99US-0158023P
PR	08-OCT-1999;	99US-0158232P
PR	12-OCT-1999;	99US-0158365P
PR	13-OCT-1999;	99US-0159283P
PR	13-OCT-1999;	99US-0159294P
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PR	14-OCT-1999;	99US-0159330P
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PR	14-OCT-1999;	99US-0159637P
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PR	21-OCT-1999;	99US-0160768P
PR	21-OCT-1999;	99US-0160770P
PR	21-OCT-1999;	99US-0160814P
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PR	22-OCT-1999;	99US-0160989P
PR	25-OCT-1999;	99US-0161404P
PR	25-OCT-1999;	99US-0161405P
PR	25-OCT-1999;	99US-0161406P
PR	26-OCT-1999;	99US-0161359P
PR	26-OCT-1999;	99US-0161360P
PR	26-OCT-1999;	99US-0161361P
PR	28-OCT-1999;	99US-0161970P
PR	28-OCT-1999;	99US-0161982P
PR	28-OCT-1999;	99US-0161993P
PR	29-OCT-1999;	99US-0162142P

Query Match	23.4%	Score 214.4;	DB 3;	Length 954;
Best Local Similarity	61.4%;	Pred. No. 6.6e-45;		
Matches 344;	Conservative 0;	Mismatches 216;	Indels 0;	Gaps 0;

QY AACCGGGGAGAAACAGGGGAGAGAGATGGGGAGGGGAAATATGATGATTAATAAAAAATTA 108

49 AAAAAAGATTTAAACAAAGAGAGAGATTTGGGAGAGGGAGATCCAGTTCAGAGAGATTA 61

Db 2 AAAAAAGATTTAAACAAAGAGAGAGATTTGGGAGAGGGAGATCCAGTTCAGAGAGATTA 61

QY GAGAAATCCGACGAGACAGCGAAGTTACATATTTCTAAAGAGAGTTGGGATCTGAAGAAG 168

109 GAGAAATCCGACGAGACAGCGAAGTTACATATTTCTAAAGAGAGTTGGGATCTGAAGAAG 168

Db 62 GAGAAATCCGACGAGACAGCGAAGTTACATATTTCTAAAGAGAGTTGGGATCTGAAGAAG 121

QY GCCAAGAGAGCTCACTGTTCTCTGTATGCTCAGAGTCTCTCATCATGTTCTTCAAGACACA 228

169 GCCAAGAGAGCTCACTGTTCTCTGTATGCTCAGAGTCTCTCATCATGTTCTTCAAGACACA 228

Db 122 GCACTAGAGCTCAACGGTTTGTGTATGCTAGGGTTTGATTTATCATGTTCTCTAGGCTCC 181

QY GGAAGTTGGCGTATTTACTGCAAGCCCTCTACTGATATTTAAGGGATATATGAGAGCTTC 288

229 GGAAGTTGGCGTATTTACTGCAAGCCCTCTACTGATATTTAAGGGATATATGAGAGCTTC 288

Db 182 AACCAAGCTTCAATGATATATATACAGCCCTTAACACACACAGAAAGAAATCTGAATCTGTAC 241

QY CAGGTTTGACTGTGAATGATCTTATGAGATGCTCAGTATGAGAGAGATGCAGATATCGCTTG 348

289 CAGGTTTGACTGTGAATGATCTTATGAGATGCTCAGTATGAGAGAGATGCAGATATCGCTTG 348

Db 242 CAAACTATTTCGATGTCGATGTTTGGGCACTCAATATAGCGAATGCAGAAACCAAG 301
Qy 349 AAGCATCTGAATGAGTTTAAACCAAACTGAGAGAGATTGAGAGAGAGGCGGAG 408
Db 302 AGGAAACTTTGGAGCAATGAGAAATCTCCGAGCTCAATCAACAGAGGCTAGGTGAG 361
Qy 409 GAATTGGAGGCGATGAGCACTAAAGCACTGCCGCTCTTGAGCAAACTTTGGAAGAGCT 468
Db 362 TCTTTGAGAGAGCTTGACATTCAGAGAGCTGCTGCTCTTGAGAGTGAATGGAACACT 421
Qy 469 CTTAAGATTGTTAGGATGAGAAAGTATCATGATCGCCACAACAACTGACACTTACAG 528
Db 422 TTCAAACTGTTGCGAGGCGCAAGTTCAATCTTTGGGAATCAGATCGAGCCACAG 481
Qy 529 AAAAGCTTAAAGCAACAGGAACTTACCGGCTCTAATCATGAACTGATATGAA 588
Db 482 AAAAGAGCAAAAGTCACACAGACATACAAAAGAAATCATATGAGACTGGAACCTAGA 541
Qy 589 GAGGAGAAATCCGAACTACCG 608
Db 542 GCTGAAGATCCTCACTATGG 561

RESULT 11

AAC51790

ID AAC51790 standard; DNA; 1170 BP.

XX AAC51790;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 69758.

XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

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 PR 29-OCT-1999; 99US-0162142P.

Query Match 23.3%; Score 213.8; DB 3; Length 1170;
 Best Local Similarity 60.3%; Pred. No. 1e-44;
 Matches 353; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

QY 24 AAGAGAGGTTGAGACAGAGAAAACGGGAGAACGGGAGAGAGATGGGAG 83
 DB 201 AAGGAAAGGTCATTAAGCCAAAGTCTTTTACAAAGTATGAGAGAAATTTGGGAG 260
 QY 84 GGGGAAGATAGATATAAAGATAGAGATCCGAGAACGGCAAGTTATCATATTTCTAA 143
 DB 261 AGGGAAGATCCATATCAAGAGATAGAGAACAGAACAGAACAGACAGTATTCATA 320
 QY 144 GAGAGAGTTGGATATCTGAGAGAGCCAGAGCTCATCTTCTCTGTATGCTCAGGT 203
 DB 321 GAGAGAAATGCTTTATTCAAGAAACACATGAGCTCACGGTTTGTGTATCTAGGT 380
 QY 204 CTCTCATCATGTTCTCAAGCAGAGAAAGTTGGGATTTACTGACGCCCTCTACTGA 263
 DB 381 TTGATTTATCATGTTCTTCTAGCTCAAGAGCTTCATGATATATACGCCCTTAACAC 440
 QY 264 TATTAAGGGATATATAGAGAGTACCAAGTTGTGACTGAGATGATCTATGAAATGCTCA 323
 DB 441 AAGGAAGAGATGATGATCTGATACCAACTATTTCTGATGTTGGGCACTCA 500
 QY 324 GTATGAGAGATGCAAGATTCGCTGAAGCTTGAATGAGATTACCAAACTGAGGA 383
 DB 501 ATATGAGCGATCAAGAAACCAAGAGAACTGTGAGACAAATAGAAATCTCCGAC 560
 QY 384 CGAGATTTAGAGAGAGAGAGGAGGAATTTGAGGCGATGACATTAAGCAATGGCGG 443
 DB 561 TCAGATCAAGCAGAGCTAGTATGTTGGCAAGCTTGACATTCAGAGCTGACCTCG 620
 QY 444 TCTTGAGCAAACTTTGAGAGAGTCTCTAGAAATTTGAGGATAGAAAGTATCATGTAT 503
 DB 621 TCTTGAGGATGAATGAGAAACCTTTCAAACTCGTTCCGAGCGCAAGTTCAATCTCT 680
 QY 504 CGCCACAAACTGACATTTACAGAAAAGCTTTAAAGCACAAGGAAACTTACCGCCG 563
 DB 681 TGGGAATCAGATGAGACCAACCAAGAAAGAAAGCAAAAGTCAACAGACATACAAAGAA 740
 QY 564 TCTAATACATGAACTGGATATGAAAGAGATCCGAATACGATACG 608
 DB 741 TCTCATACATGAGCTGAACTAAGCTGAAATCTCACTATGG 785

RESULT 12
 ADO61550 standard; DNA; 988 BP.
 ADO61550;

15-JUL-2004 (first entry)

DE Transcription factor G133 coding sequence, SEQ ID 17.

XX Plant; transcriptions factor; transgenic plant; abiotic stress tolerance;
 XX osmotic stress tolerance; cold tolerance; heat tolerance;
 XX low nitrogen tolerance; low phosphate tolerance; fungal disease;
 XX glyphosate resistance; flowering; fertility; seed development; de.

OS Arabidopsis thaliana.

PN WO2004031349-A2.

PD 15-APR-2004.

XX

PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
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Db	366	CTGCGCTGCTCTTGAGGATGAAATGGAAAAACATTTTCAAACTGTTCCGAGACGGACGCTTC	425
Qy	496	CATGTATGCGCCACAAACACACCTTAACAAGAAAAAGCTTAAAGCACAAAGGAACCT	555
Db	426	AAATCTCTTGGGAGATCAGATCGAGACACCAAGAAAAAGAACAAAGTCAACAAAGACTA	485
Qy	556	TACCGGCTCTAATACATGAACCTGGATATGAAAAGAGAGAAATCCGAATTACGG	608
Db	486	CAAAAGATCTCATACATGATGAGTGGAACTMAAGCTGAAGATCTCTCACTATGG	538

RESULT 15
ADK59635
ID ADK59635 standard; DNA; 665 BP

ADK59635 ; AC

DT 06-MAY-2004 (first entry)

DE Plant DNA sequence which confers altered metabolic characteristic #7018.

KW altered metabolic characteristic; plant; acid metabolism, alcohol metabolism, fatty acid metabolism.

KW branched fatty acid metabolism; alkaloid metabolism; amino acid metabolism; ether metabolism; glucoside metabolism

KW phenolic metabolism; carbohydrate metabolism; steroid metabolism
KW formate metabolism; alkene metabolism

KW alkynes metabolism; hydrocarbon metabolism; ketone metabolism;
KW amino acid metabolism; dicarboxylic acid catabolism; ncp; ds

Unidentified

PN WO2003020936-A1

PD 13-MAR-2003

PF 30-AUG-2002; 2002WO-US027884.

PR 31-AUG-2001; 2001US-0316471P.

PA (DOMC) DOM CHEM CO.

XX

PI Oriedo JVB, Crosley R, Reddy AS, Shukla V, Larrinua I, Miller BA,

DR WPI; 2003-313091/30.

PT Novel genes that confer altered metabolic characteristics in *Nicotiana glauca* plants useful for altering the levels of metabolites in *N. glauca* plants

PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols

PS Claim 1; SEQ ID NO 7018; 2576pp; English
XY

CC The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of

CC the invention are useful for producing plants with an altered metabolic
CC characterisatic such as: altered acid metabolism, alcohol metabolism, or

CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
CC have metabolism altered amino acid metabolism altered ester metabolism

CC altered glyceride metabolism, altered phenolic metabolism, altered
CC carbohydrate metabolism altered steroid oxygenated terpene or

CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
CC metabolism or ketone metabolism The DNA sequences of the
CC metabolism or quinone metabolism

CC invention may be used to provide disease resistance in a plant and gene
CC shuffling or sexual PCR procedures. The present nucleic acid represents a

CC DNA sequence of the invention.
XX

sequence 665 BP; 224 A; 144 C; 152 G; 145 T; 0 U; 0 Other

Query Match	22.9%;	Score 209.8;	DB 10;	Length 665;
Best Local Similarity	62.1%;	Pred. No. 8.8e-44;		
Matches 331;	Conservative 0;	Mismatches 202;	Indels 0;	Gaps 0;

Oy	76	ATGGGAGAGGGGAAAGATAGAGATTAATAAAAAAGATAGAGAAATCCAGCAAGAACGACGATTAACA	135
Db	6	ATGGGAGAGGGGAAAGATCCAGATCAAAAGGATATAGAAACCAAGACAAACAGACAAGTGACG	65
Oy	136	TATTTCTAAGAGAGAGTTGGGATACTGAAAGAGCGCCAGAGACTCACTTTCTCTGTGAT	125
Db	66	TATTCAAAGAAAGAAATGGTTTATTATCAAGAAAGACATGAGACTCACGGTTTTGTGTGAT	125
Oy	196	GCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAAGTTGGCTGATTAAGTCACAGCCC	255
Db	126	GCTAGGGTTTGATATATCATGTTCTTACGCTCCAAACAGCTTCATATGATATATACGCCCT	185
Oy	256	TCTACTGATATTTAAGGGGATATATGAGAGATACCAAGTTGTGACTGGAATTCGATCTATGG	315
Db	186	AACACCAACAAAGAAAGAGATCGTAATCTGTACCAACATATTTCTGATGTGATGTTTGG	245
Oy	316	AATGCTCAGTATGAGAGATGAGAAATCGCTGAAGCATCTGATATGATTAACAAAAC	375
Db	246	GCCACTCATATGACCGAAATGCAGAAACCAAGAGAAACTGTTGAGACAAATATAGAAAT	305
Oy	376	CTGAGGAAGAGATTAGAGAGAGAAAGGGGAGAAATGGAGGCGCATGACATTAAGCAA	435
Db	306	CTCCGGATCTCAGATCAACAGAGCGCTAGAGTGAATTTTGGACAGACTTGACATTCAGGAG	365
Oy	436	CTGGCGGCTCTTGAGCAAACTTTGGAAAGATCTCTTGAATTGTTAGGATATGAAAGTAT	495
Db	366	CTGGCTGCTTTGAGGATGAAATGGAATACCTTTCAAACTGTTTGGCGAGCGCAAGTTTC	425
Oy	496	CATGTGATCGCCACAACAACTGACCTTACAAGAAAAAGCTTTAAAGCAACAAAGGAACT	555
Db	426	AAATCTTTGGGAATCAGATCGAGACCAACCAAGAAAAAGAACAAAGATCAACAAAGCATTA	485
Oy	556	TACCGCGCTCAATATCATGAATCTGGAATATGAAGAAGAGAAATCCGAACTTACAGG	608
Db	486	CAAAAGATTCATATCATGATGCTGGAACTTAAGAGCTGAAGATCTTCACATTATGG	538

Search completed: February 1, 2005, 21:51:26
Job time : 421 secs


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QY 121 AACGAGAAAGTAACTATTTCTAAAGAGAGATTGGATATCTGAAGAGGCCAAGAGCTC 180
Db 121 AACGAGAAAGTAACTATTTCTAAAGAGAGATTGGATATCTGAAGAGGCCAAGAGCTC 180
QY 181 ACTGTTCTGTGATGTCAGAGTCTCTCATCATGTTTCTCAAGACAAGAAAGTTGCT 240
Db 181 ACTGTTCTGTGATGTCAGAGTCTCTCATCATGTTTCTCAAGACAAGAAAGTTGCT 240
QY 241 GATTACGAGAGCCCTCTACTGATTTAAAGGATATAGAGGTACCAAGTTGTACT 300
Db 241 GATTACGAGAGCCCTCTACTGATTTAAAGGATATAGAGGTACCAAGTTGTACT 300
QY 301 GGAATGATCTATGGAATGCTCAGATATAGAGATGAGAAATACCTGAACATCTGAAT 360
Db 301 GGAATGATCTATGGAATGCTCAGATATAGAGATGAGAAATACCTGAACATCTGAAT 360
QY 361 GAGATTTAACCAACCTGAGAGAGATTTAGAGAGAGAGAGAGAAATTTGAGAGGC 420
Db 361 GAGATTTAACCAACCTGAGAGAGATTTAGAGAGAGAGAGAGAAATTTGAGAGGC 420
QY 421 ATGACATTAAGCAACTGCGGCTTGAAGCACTTTGAAAGTCTTTAGAAATGTT 480
Db 421 ATGACATTAAGCAACTGCGGCTTGAAGCACTTTGAAAGTCTTTAGAAATGTT 480
QY 481 AGGCATGAAGATATCATGATGTCGACACAACTGACACTTACAAAGAAAGCTTAA 540
Db 481 AGGCATGAAGATATCATGATGTCGACACAACTGACACTTACAAAGAAAGCTTAA 540
QY 541 AGCAGAGGAGAACTTACCGGCTTAAATCATGAATGAGATATGAGAGAGATCG 600
Db 541 AGCAGAGGAGAACTTACCGGCTTAAATCATGAATGAGATATGAGAGAGATCG 600
QY 601 AACTACGTTTTATGAGAGAAACAGAGATGAATTTAGAAATTCATTCATGAGTG 660
Db 601 AACTACGTTTTATGAGAGAAACAGAGATGAATTTAGAAATTCATTCATGAGTG 660
QY 661 AATGATGTCCTCAGATGTTTTCTTTAGAGGTTGTCATCCGAATCAGCCCATCTCT 720
Db 661 AATGATGTCCTCAGATGTTTTCTTTAGAGGTTGTCATCCGAATCAGCCCATCTCT 720
QY 721 GGTTAGTTATGATCATCATGATCTTACCTTGATATGAGAGATATATGATTT 780
Db 721 GGTTAGTTATGATCATCATGATCTTACCTTGATATGAGAGATATATGATTT 780
QY 781 TATTTGATTTTATTTATGTTTGAACCTTGAATTAAGATGAGAGATATATGATTT 840
Db 781 TATTTGATTTTATTTATGTTTGAACCTTGAATTAAGATGAGAGATATATGATTT 840
QY 841 GAGAACTGCTCTTAATTTGATTTCCCGTTTGTTCCTTCATGTCAGTGAATTTT 900
Db 841 GAGAACTGCTCTTAATTTGATTTCCCGTTTGTTCCTTCATGTCAGTGAATTTT 900
QY 901 TTGTTTTGTTTTTCGG 917
Db 901 TTGTTTTGTTTTTCGG 917

```

RESULT 2
US-10-690-246-7

```

; Sequence 7, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, WEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2

```

```

; SEQ ID NO 7
; LENGTH: 898
; TYPE: DNA
; ORGANISM: Phalaenopsis equestris
; NAME/KEY: CDS
; LOCATION: (123) .. (782)
US-10-690-246-7

```

Query Match 39.0%; Score 357.6; DB 18; Length 898;
Best Local Similarity 75.7%; Pred. No. 5, 8e-84;
Matches 457; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

```

QY 76 ATGGGAGAGGAGAGATAGATATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 135
Db 123 ATGGGAGAGAGAGAGATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAG 182
QY 136 TATTTAAGAGAGAGATTTGAGATCTGAAGAAAGCCAGAGAGCTCACTGTTCTGTGAT 195
Db 183 TATTTAAGAGAGAGAGATTTGAGATCTGAAGAAAGCCAGAGAGCTCACTGTTCTGTGAT 242
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGCTGATTAAGAGCC 255
Db 243 GCTCAACTCTCATCATCATCTTCTCAAGCTCCGCAAGTTAGCTGATTTCTGAGCCCT 302
QY 256 TCTACTGATATTAAGGAGATATAGAGATGACAGAGTTGTAAGTGAATGATGATG 315
Db 303 TCCACAGAGCTTAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 362
QY 316 AATGCTCAGATATGAGAGATGACAGATTCGTTGAAGATCTGAATGATTAAGCAAAAC 375
Db 363 GATGGGCAATATCAGAGAGATGACAGATCTGAGATCTGAGAGATTAATTCGTAAT 422
QY 376 CTGAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 435
Db 423 CTTCAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
QY 436 CTGGCGGCTCTTGAAGCACTTTGAAAGAGTCTCTTAAGATTTGTTAGCATTAAGAG 495
Db 483 CTGGCGGCTCTTGAAGCACTTTGAAAGAGTCTCTTAAGATTTGTTAGCATTAAGAG 542
QY 496 CATGATGTCGACACAACTGACACTTACAAAGAAAGCTTTAAAGACAGAGAGAACT 555
Db 543 CATGATGTCGACACAACTGACACTTACAAAGAAAGCTTTAAAGACAGAGAGAACT 602
QY 556 TACCGGCTCTAATACATGATGATGATA---TGAAAGAGAGAGAAATCCGAATCAGGTTT 612
Db 603 TACAGAGCCCTTAACGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 662
QY 613 AATGTAAGAAACAGAGATTAATTAAGAAATTCGATTCATGATGATGATGATGATG 672
Db 663 CTGTGAAGATCTAAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 722
QY 673 CAGA 676
Db 723 CCGA 726

```

RESULT 3

```

US-10-690-246-5
; Sequence 5, Application US/10690246
; Publication No. US20040210967A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, HONG-HWA
; APPLICANT: TSAI, WEN-CHIEH
; TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
; FILE REFERENCE: U 014863-8
; CURRENT APPLICATION NUMBER: US/10/690,246
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: 091125320
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2

```


SEQ ID NO 5
LENGTH: 1036
TYPE: DNA
ORGANISM: Phalaenopsis equestris
FEATURE:
NAME/KEY: CDS
LOCATION: (216)..(887)
US-10-690-246-5

Query Match 35.4%; Score 324.2; DB 18; Length 1036;
Best Local Similarity 69.1%; Pred. No. 4.3e-75;
Matches 475; Conservative 0; Mismatches 203; Indels 9; Gaps 2;

QY 74 AGATGGGAGGAGGAGATGAGATTAAGGATGAGATCCGACCAAGCAAGTTA 133
DB 214 AGATGGGAGGAGGAGATGAGATTAAGGATGAGATCCGACCAAGTTA 273
QY 134 CATATTCTAAGAGAGAGTGGGATCTGAAGAGCCCAAGAGCTCCTCTGTG 193
DB 274 CTTACTGAGAGAGAGAGCTGGGATTAAGAGAGGCGAGAGATCCTGTTCTGCG 333
QY 194 ATGCTGAGTCTCTCATCATGTTCTCAAGCAAGAGAGTTGGCTGATTCTGACCC 253
DB 334 ATGCTGAGTCTCTCATCATGTTCTCAAGCAAGAGAGTTGGCTGATTCTGACCC 393
QY 254 CCTCTATGATTAAGGAGATTAAGAGAGTACCAAGTTGCTGACTGGAATGATCTAT 313
DB 394 CTTGAGAGGAGAGAGAGTTTGAAGGCTACCAAGAGTATCTGGCATTAAGTTGT 453
QY 314 GGAATGCTGATGAGAGATGAGATTAAGGCTGAAGCATGGAATGAATTAAGCAAA 373
DB 454 GGAAGCTGAGTACGAGAGATGCTGAATTCCTTAAGCATGGAATGAATTAAGCA 513
QY 374 ACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAGCA 433
DB 514 ATCTGAGAGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGATTAAGCA 573
QY 434 AACTGCGCGCTCTTGAAGCAAGTTGAGAGAGTCTCTTAAGATTTGTTAGCATTAAG 493
DB 574 AACTGCGCGCTCTTGAAGCAAGTTGAGAGAGTCTCTTAAGATTTGTTAGCATTAAG 633
QY 494 ATCATGATGATGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGAGAG 553
DB 634 ATCATGATGATGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGAGAG 693
QY 554 CTTACCGCGCTCTTAATATGAAGTGAAGAGAGAGAGAGAGAGATTAAGAGAGAG 613
DB 694 CACACGGAAGTTAATGAGAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAG 753
QY 614 ATGTAGAAAACAGAGATTAAGAGAGAGAGAGAGAGATTAAGAGAGAGAGAG 673
DB 754 ACG-----AGATTAAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAG 807
QY 674 AGATGTTTCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 733
DB 808 AACTGATGCTCTTCCG---GTGCAACCCCAAGCAAGAGAGAGAGAGAGAGAGAG 864
QY 734 AATCATGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 760
DB 865 GCTCTCAGCATCTTCCCTGCTTGAAT 891

RESULT 4
US-10-690-246-3
Sequence 3, Application US/10690246
Publication No. US20040210967A1
GENERAL INFORMATION:
APPLICANT: CHEN, HONG-HWA
APPLICANT: TSAI, WEN-CHIEH
TITLE OF INVENTION: GENES FOR CONTROLLING FLORAL DEVELOPMENT IN ORCHID
FILE REFERENCE: U 014863-8
CURRENT APPLICATION NUMBER: US/10/690,246
CURRENT FILING DATE: 2003-10-21

PRIOR APPLICATION NUMBER: 091125320
PRIOR FILING DATE: 2002-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 980
TYPE: DNA
ORGANISM: Phalaenopsis equestris
FEATURE:
NAME/KEY: CDS
LOCATION: (196)..(864)
US-10-690-246-3

Query Match 34.5%; Score 316.8; DB 18; Length 980;
Best Local Similarity 65.3%; Pred. No. 3.8e-73;
Matches 503; Conservative 0; Mismatches 252; Indels 15; Gaps 2;

QY 65 GGAAGAGAGAGAGAGGAGGAGAGATGAGATTAAGAGAGAGATTAAGAGAGAGAG 124
DB 185 GGAAGAGAGAGAGAGGAGGAGAGATGAGATTAAGAGAGAGATTAAGAGAGAGAG 244
QY 125 GGCAGTTATATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 184
DB 245 GGCAGTTATCTTAAG 304
QY 185 TTCTCTGATGCTCAGGCTCTCTCATCATGTTCTCAAGCAAGAGAGAGAGAG 244
DB 305 TTCTCTGATGCTCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 364
QY 245 ACTGAGCCCTCTCATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 304
DB 365 ATTTGATGCTCTACACAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 424
QY 305 TGGATTAAG 364
DB 425 TAAATTTAAG 484
QY 365 TTAAACCAAACTGAG 424
DB 485 TAAACCAAACTGAG 544
QY 425 ACATTAAG 484
DB 545 AAATCAAG 604
QY 485 ATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 544
DB 605 ATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 664
QY 545 CAAAG 604
DB 665 CTTCAAG 712
QY 605 AGCGTTTATGAG 664
DB 713 CGGTCTACAG 772
QY 665 AGTGTCTGAG 724
DB 773 GGGCTTCTACAG 829
QY 725 TAGGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 784
DB 830 TTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
QY 785 GATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 834
DB 890 CTTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 939

RESULT 5
US-10-260-238-5530
Sequence 5530, Application US/10260238

```

; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
; APPLICANT: Mounhamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyuki
; APPLICANT: Krepes, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Rieke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 5530
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Zea mays
US-10-260-238-5530

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Query Match      25.6%; Score 234.8; DB 16; Length 681;
Best Local Similarity 65.8%; Pred. No. 1.6e-51;
Matches 341; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

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QY 76 ATGGGAGGGGGAAGATAGATATAAAGATGAGATCCAGCAAGCAAGGATTACA 135
DB 1 ATGGGGGCGCGCAAGATCGAGATCAAGCGATGAGAACGCCAACCGCAAGTACC 60
QY 136 TATCTAAGAGAGAGTTGGATCTGAAAGAGCCCAAGAGCTCATGTTCTTGAT 195
DB 61 TACTCCAGGCGCGGAGCGGAGATCAAGAGAGCGCGGAGCTCACGTCCTGAGAC 120
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAAGAGCCC 255
DB 121 GCCCAGGTGCGCATCTCATGTTCTCTCCACCGCAAGTACCAAGATTCTGACGCC 180
QY 256 TCTACTGATATTAAGGGATATATAGAGGTACCAAGTTGTACTGGAATGATCTATGG 315
DB 181 GGAACCGACATCAACCATCTTGAACCGGTACCAAGGCAATCCGAGCAAGCTATGG 240
QY 316 AATGCTCAGTATGAGAGATCAGAAATACGCTGAAGCATCTGATGATTAACCAAAAC 375
DB 241 ATCGACAGTATGAGAAATATGACGCGACCGTACCAAGCAATCAATCATGCTGAT 300
QY 376 CTGAGGAAGAGATTAGAGAGAGAGAGAGAGAAATTGAGGCAATGACATTAAGCAA 435
DB 301 CTGGGCAAGAGATTAGCAAGAAAGAGAGAGAGATCTGACATCTGGAATTCGACGAG 360
QY 436 CTGGCGGCTCTTAGCAAACTTTGAAAGATCTTTAAGATTGTTAGGATAGAAAGTAT 495
DB 361 CTGGCGGCTCTGAGCAAAACGTCGACGCGGCTCTCAAGAGATTGCGCATAGGAATAC 420
QY 496 CATGTATGCCACACAAATGACACTTACAAAGAAAAGCTTTAAAGCACAAGGAAACT 555
DB 421 CATGTATCAGACGACGACTGATACCTACAAAGAAAAGGTAAGCACTCGACAGAGCG 480
QY 556 TACCGGCTCTTAATCATGAATGGAATGGAAGAGA 593
DB 481 TACAAGAACTTCAAGAGAGCTAGGCAATGCGGAGAGA 518

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RESULT 6
US-10-104-580-2

```

; Sequence 2, Application US/10104580
; Publication No. US20030033628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 946
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
US-10-104-580-2

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```

Query Match      24.9%; Score 228; DB 14; Length 946;
Best Local Similarity 58.3%; Pred. No. 1.2e-49;
Matches 399; Conservative 0; Mismatches 285; Indels 0; Gaps 0;

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QY 76 ATGGGAGGGGGAAGATAGATATAAAGATGAGATCCAGCAAGCAAGGATTACA 135
DB 1 ATGGGGTGTGAAAGATTGAAATAGAAAGATGAAAAACCCACAAACGCAAGTACC 60
QY 136 TATCTAAGAGAGAGTTGGATCTGAAAGAGCCCAAGAGCTCATGTTCTTGAT 195
DB 61 TACTCCAGGAGAAAGATGATATTTCAGAAAGCCCAAGCAATCATGTAATTTGAT 120
QY 196 GCTCAGGTCTCTCATCATGTTCTCAAGCAGAGAAAGTTGGCTGATTAAGAGCCC 255
DB 121 GCTAAGGTCTCTTATCATGTTCTCCACCACTAACTCAATGATGATATGATAGCCC 180
QY 256 TCTACTGATATTAAGGGATATATAGAGGTACCAAGTTGTACTGGAATGATCTATGG 315
DB 181 TCCACATCAACAAAGATATACGATCATATATCAAGACCTTTAGGATATGATGG 240
QY 316 AATGCTCAGTATGAGAGATCAGAAATACGCTGAAGCATCTGATGATTAACCAAAAC 375
DB 241 GGCACCTCATACGAAATATCCAGAGCACTTGAGAAAGCTGAATGATATCAATCATAG 300
QY 376 CTGAGGAAGAGATTAGAGAGAGAGAGAGAGAAATTGAGGCAATGACATTAAGCAA 435
DB 301 CTGAAACAAGAAATCAGCAGAGAGAGAGAGAGGCTGAAATGATCTGACATTAATCAT 360
QY 436 CTGGCGGCTCTTAGCAAACTTTGAAAGATCTTTAAGATTGTTAGGATAGAAAGTAT 495
DB 361 CTGGCGGCTCTTGAACAATATGACATGAAAGCTTGAATGATGCTGGGAGAGAGTAC 420
QY 496 CATGTATGCCACACAACTGACACTTACAAAGAAAAGCTTTAAAGCACAAGGAAACT 555
DB 421 CATGTATCAAAACAAACAAACCTACAGAGAAAGGTAAGAAATTTAGAGAGAGA 480
QY 556 TACCGGCTCTTAATCATGAATGGAATGGAAGAGA 593
DB 481 CATGAAGAACTCTTATGAGAAATTTAGAAATTCGATGATGATGATGATGATGATGAT 615
QY 616 GTAGAAACCAAGATGATATTAAGAAATTCGATGATGATGATGATGATGATGATGAT 675
DB 541 GACAATGAAAGCTGCTGACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 676 ATGTTTCTTTAGGATTTGATCCGAATCAGCCCAATGCTGCTTGAATGATGATGAT 735
DB 601 CATCAGGAGCAACACACACACATCTCTTAATCTTCACTTGAAGATGATTTGGA 660

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QY 736 TCACATGATCTTAGCCTTGATTA 759
DB 661 GCCCATGAACCTTGCCCTTGGA 684

RESULT 7

US-10-104-580-3
; Sequence 3, Application US/10104580
; Publication No. US2003003628A1
; GENERAL INFORMATION:
; APPLICANT: Straus et al.
; TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in poplar and other plant species.
; FILE REFERENCE: 62486
; CURRENT APPLICATION NUMBER: US/10/104,580
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 09/410,464
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 09/287,700
; PRIOR FILING DATE: 1999-04-06
; PRIOR APPLICATION NUMBER: 60/080,851
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(681)
US-10-104-580-3

Query Match 24.8%; Score 227.2; DB 14; Length 681;
Best Local Similarity 58.4%; Pred. No. 1.6e-49;
Matches 397; Conservative 0; Mismatches 283; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAATAGAGATTAATAAGATAGAGATCGAGCAAGCAAGCAAGTTACA 135
DB 1 ATGGGCTGCGGAAGATTGAATCAAGAGATCGAAGAACCCCAACAGCAAGCAAGTACC 60
QY 136 TATCTTAAGAGAGATGGGATCTAGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
DB 61 TACTCAAG 120
QY 196 GCTCAGAGTCTCTCTCATCATGTTCTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
DB 121 GCTAAGTCTCTCTCTCATCATGTTCTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 256 TCTACTGATATTAAAGGGGATATAGAGAGTACCAAGTTGATCTGGAATGATCTAATGG 315
DB 181 TCACATCGACAAAGAGATCTACGATCAATATCAGAACCTTTAAGGCATAGATCTGTGG 240
QY 316 AATGCTCAGATATAG 375
DB 241 GGCACCTCAATACAGAAAGATGCAAGAGCATTGAGAGAGCTGATGATCAATCAATAG 300
QY 376 CTGAGAGAGAGATTAAG 435
DB 301 CTGAG 360
QY 436 CTGCGGCGCTTTGAG 495
DB 361 CTGCGGCGCTTTGAG 420
QY 496 CAGTGTATGCGCCACACAAATGACATTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555
DB 421 CAGTGTATGCGCCACACAAATGACATTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 556 TACCGGCTCTTAATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 615
DB 481 CAGTGTATGCGCCACACAAATGACATTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540

QY 616 GTAGAAACCAAGTAGAATTTATGAATAATTCGATTCGATGATGATGATGATGATGAT 675
DB 541 GACAAATGAAGCTGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 676 ATGTTTCTTTAGGGGTTGTTGATCCGAAATCAGCCCAATCTGCTGTTAGTTAGTAA 735
DB 601 CATCAGGGGAC 660
QY 736 TCACATGATCTTAGCCTTG 755
DB 661 GCCCATGAACCTTGCCCTTG 680

RESULT 8

US-10-856-499-10
; Sequence 10, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Modifications and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: PasterSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-10

Query Match 23.6%; Score 216.6; DB 18; Length 989;
Best Local Similarity 64.4%; Pred. No. 1.3e-46;
Matches 324; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

QY 73 GAGATGGGGGAGGGAATAGAGATTAATAAGATAGAGATCGAGCAAGCAAGTTACA 132
DB 4 GAGATGGGGGAGGGAATAGAGATTAATAAGATAGAGATCGAGCAAGCAAGTTACA 63
QY 133 ACATATTTTAAAG 192
DB 64 ACCTACTCGAAGGAG 123
QY 193 GATGCTCAGGCTCTCTCATCATGTTCTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 252
DB 124 GACCCCAAGGCTCTCATCATGATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 183
QY 253 CCTCTACTGATATTAAAGGGGATATAGAGAGTACCAAGTTGATCTGGAATGATCTA 312
DB 184 CCTCTACTGATATTAAAGGGGATATAGAGAGTACCAAGTTGATCTGGAATGATCTA 243
QY 313 TGAATGCTCAGTATAGAGAGATGCAATACGCTGAAGCATGTAATGATTAACCA 372
DB 244 TGAAGCTCTCATATAGAGAGATGCAATACGCTGAAGCATGTAATGATTAACCA 303
QY 373 AACCTGAGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
DB 304 AACCTGAGAGAGATTAAG 363
QY 433 CAATCGCGGCTTTGAG 492
DB 364 GATTTGCGGCTTTGAG 423
QY 493 TATCATGATGCGCCACACAAATGACATTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 552
DB 424 TACAAAGAGCTTGGCAGATCAATGACACCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 483
QY 553 ACTTACCGGCTCTTAATACATGA 575


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; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10670
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700958586_FLI
US-10-425-114-10670

Query Match      22.0%; Score 202; DB 16; Length 871;
Best Local Similarity 62.1%; Pred. No. 8,8e-43;
Matches 319; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 86 GGAAGTAGAGATAAAGATAGAGATCCGACGAACAGGCAAGTTACTATTCTTAAGA 145
DB 1 GAAAGATCCAGATCAAGAGATAGAGAACACACCAACCCGACCTTATTCTTAAC 60
QY 146 GGAGAGTGGGATCTGAGAGAGCCAGAGCTCACTGTTCTGTGATGTCAGAGTCT 205
DB 61 GAGGAGATGGCCCTTTTCAGAGAGCCAGAGCTCACTGTTCTGTGATGTCAGAGTCT 120
QY 206 CTCTCATCATGTTCTCAAGACAGAGAAAGTTGCTGATTAAGTCAAGCCCTCTACTGATA 265
DB 121 CTATTATATATGTTCTCAGACAGTGGAAACTCCACAGATCATCAGCCCTCCACCTCAA 180
QY 266 TTAAGGGGATATATGAGAGTACCAAGTGTGTGACTGGAATGATCTATGAAATGCTCAGT 325
DB 181 CAAAGAGTCTTCGATCAGTACCAATGATCTCTAGAGTGCATCTCTGAACTCTCATT 240
QY 326 ATGAGAGATGCGAATACGCTGAGCATCTGAATGATTAACCAAACTGAGGAAG 385
DB 241 ACGAGATATGCAAGAGAACTTGAAGAACTCAAAATGTGAATAGGAATCTTCTGAAG 300
QY 386 AGATTAGAGAGAGAGAGGAGGAGAAATGAGAGGCAATGAATGAACCACTGCGGCTC 445
DB 301 AGATTAGAGAGAGATGGAGATTGTCTGAACGATCTGGGCTATGGAAGATCTCAAGCTCC 360
QY 446 TTGAGCAAACTTTGGAAGAGTCTCTTGAATTTTGAAGCATTAAGAAATGATCATGTATCG 505
DB 361 TTGAGGAAAGAAATGACAAAGCGCCGCAAGGTTGTTGTTGAACGTAAAGTATAGGTATTA 420
QY 506 CCACACAAACCTGACACTTCAAGAAAAAGCTTAAAGCAAGGAAACTTACCGGCTC 565
DB 421 CAAATATAGATGACACCCAAAGAAAAAGTTTAATTAACGAGAAAGAGTGCACAAAGAC 480
QY 566 TAATACATGAACTGATATGAAAGAGAGAAATCC 599
DB 481 TCCTGCGTACTTGATGCAAGAGCAAGATGCC 514

RESULT 12
US-09-732-627A-4479
; Sequence 4479; Application US/09732627A
; Publication No. US2004012338A1
; GENERAL INFORMATION:
; APPLICANT: Fitcher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5170)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4930
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; SEQ ID NO 4479
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; NAME/KEY: unsure
; LOCATION: (1)-(498)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB3493-034-PL-M1-H12
US-09-732-627A-4479

Query Match      21.9%; Score 201.2; DB 11; Length 498;
Best Local Similarity 64.6%; Pred. No. 1.1e-42;
Matches 299; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

QY 76 ATGGGAGGGGGAAGATAGAGATAAAAAGATAGAGATCCGACGAACAGGCAAGTTACA 135
DB 25 ATGGCTCGAGGGAATCCAGATCAAGCTGATGAGAACTTCGACCAAGGCAAGTCACG 84
QY 136 TATTCTAAGAGAGATTTGGATCTGAAAGAGCCCAAGAGCTCATGTTCTGTGAT 195
DB 85 TATTGGAAGAGAGAAACGATCTTTTCAGAAAGCTTAATGAACTTACAGTTCTTTCGAT 144
QY 196 GCTCAGGCTCTCTCATCATGTTCTCAAGACAGAAAGTTGGCTGATTAAGTCAAGCC 255
DB 145 GCTAAGTTCATCATCATGTTCTTTCACACTGATGTAAGTCCATGATTTACAGCCCT 204
QY 256 TCTACTGATATTAAGGGATATATGAGAGTACAGAGTTGTGACTGGAATGATCTATGG 315
DB 205 TCCACCAACAAGAAAGAAATGATGATCAGTACAGAAACCTTGGGAGATCATCTGG 264
QY 316 AATGCTCAGTATGAGAGATGCAAGTACGCTGAACATCTGAATGATTAACCAAAAC 375
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DB 325 CTGCGCAAGAGATTGAGAGAGAGTGGCGACTGTTGAATATTTGAGCATCGAAGAT 364
QY 436 CTGCGGCGTCTTGAGCAAACTTTGGAAGAGTCTCTTGAATTTTGAAGCATAGAAATAT 495
DB 385 CTGAGTCTTGGAACAAGAAATGAGAGCTGTGACACTTATTTGCTGATAGAAATAT 444
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DB 445 CGTGTCTCTCCAAACCAATCATCTTACAGAAAAAAGTGA 487

RESULT 13
US-10-425-114-15025
; Sequence 15025; Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 15025
; LENGTH: 1231
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3049-050-F6_FLI
US-10-425-114-15025
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Db      229 GAGATGGGTGCTGCGAAGATTGAGATTAAGTTGATTGAGAAACCCACCAACAGGCAAGTC 288
QY      133 ACAATATTCTAAGAGAGAGATTGGGAAATCTGAAGAGGCCAAGAGCTCACTGTTCTCTGT 192
Db      289 ACCTACTCCAGAGGAGGAAATGGTATCTTCAAGAAAGCTCATGAACTCAGTGTCTCTGT 348
QY      193 GATGCTCAGGCTCTCTCATCATGTTCTCAAGCACAGAAAGTTGCGTGAATTACTGAGC 252
Db      349 GATGCCAAGGTTTCATCATCATGTTCTCTAATAAACAAACAGATGCATGAAATACATTAGC 408
QY      253 CC---CTCTACTGATATTAAAGGGATATATAGAGGTACCAAGTTGTGACTGGAAATGAT 309
Db      409 CCTGGCCTCAGCAAAAGATCATTGATCAAGTATCAGAAAGCTTTGGGGATATTGAT 468
QY      310 CTATGGAATGCTCAATATGAGAGATGCAGAATACGCTGAAGCATCTGAATGAGATTAC 369
Db      469 CTGTGCATTCTCACTATGAGAAATGCTTGAATACTTGAAGAAAGCTGAAGAATATTAC 528
QY      370 CAAACCTGAGAGAGAGATTAGAGAGAGAGGGGAGGAATTGAG-----GGCATG 423
Db      529 AATAGCTCGGAGACAGATCAGGCATAGATAGGTAGGGCTTGGACATGACGACATG 588
QY      424 GACATAAGCACTGCGGCTCTTGAGCAAACTTTGGAAGAGTCTTTAGAAATTGTAGG 483
Db      589 AGCTTCAGCAACTGCGCACTCTTGAAGAAATATGTTTCATCCATAGGAAATACGC 648
QY      484 CATAGAAAGTATCATGTGATGCGCACAAACTGACACTTACAGAAAGAAAGCTTAAAGC 543
Db      649 GAACGAAAGTTTCACGTGATCAAAACTCGGACTGATACCTGTAGGAAAGGTTAAAGC 708
QY      544 ACAAGGAAACTTACCGCGCTCTAATACATGAAC 578
Db      709 CTGAAGCAGATGAATGGAATCTGCTGCTGAAC 743

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Search completed: February 1, 2005, 23:58:52
 Job time : 587 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 1, 2005, 21:25:24 ; Search time 2952 Seconds

(without alignments)
11319.524 Million cell updates/sec

Title: US-10-690-246-1

Perfect score: 917

Sequence: 1 accgcggagatcagaggaag.....ttttgtttttttttcg 917

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_est4.*
5: gb_est5.*
6: gb_est6.*
7: gb_est7.*
8: gb_est8.*
9: gb_est9.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261.6	28.5	585	6	CB626851
2	257.8	28.1	762	6	CB971393
3	255.2	27.8	692	6	CB972246
4	250.8	27.4	694	6	CB921382
5	246	26.8	651	5	BU994760
6	238.6	26.0	645	2	BE497689
7	237.8	25.9	605	6	CA732396
8	237.2	25.7	622	6	BF291839
9	236	25.7	872	6	CD439730
10	236	25.7	1273	3	AY109302
11	232.6	25.4	605	6	CA597172
12	228	24.9	604	1	AJ803128
13	227.4	24.8	642	6	CB087977
14	226.8	24.7	605	5	BU877396
15	226.8	24.7	639	5	BU879075
16	226.8	24.7	710	5	BU875031
17	222	24.2	630	6	CA600487
18	220	24.0	757	1	AJ568207
19	220	24.0	784	1	AJ790416
20	218.4	23.8	623	1	AJ801669
21	218.2	23.7	697	1	AJ568191
22	217.6	23.7	508	5	BU878141
23	217.6	23.7	569	6	CA599518
24	215.6	23.5	722	1	AJ559554

25	214	23.3	762	1	AJ799190
26	213.2	23.2	633	6	CB078339
27	212	23.1	871	3	CNS0A722
28	212	23.1	969	3	CNS09YEO
29	211.4	23.1	624	7	CK118415
30	211.4	23.1	800	1	AJ568199
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33	206	22.5	581	5	BU880121
34	205.8	22.4	512	1	AJ797978
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36	204.8	22.3	519	1	AJ786867
37	203.2	22.2	698	2	AW737915
38	202.8	22.1	624	4	BI977629
39	201.6	22.0	652	4	BI924444
40	201.6	22.0	686	1	AJ806174
41	201.2	21.9	535	2	BF291862
42	201	21.9	567	2	AW624642
43	201	21.9	616	2	BF324502
44	201	21.8	714	4	BI929568
45	200.2	21.8	590	2	AW624717

ALIGNMENTS

RESULT 1	CB626851	585 bp	mrna	linear	EST 08-APR-2003
LOCUS	OSIIEB01G03.f	OSIIEB	Oryza sativa	(indica cultivar-group)	cdna
DEFINITION	clone OSIIEB01G03 5', mRNA sequence.				
ACCESSION	CB626851				
VERSION	CB626851.1	GI:29621840			
KEYWORDS	EST.				
SOURCE	Oryza sativa (indica cultivar-group)				
ORGANISM	Oryza sativa (indica cultivar-group)				
REFERENCE	Kandasamy, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.				
AUTHORS	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea				
TITLE	Unpublished (2003)				
JOURNAL	Contact: Rod Wing				
COMMENT	Arizona Genomics Institute				
	University of Arizona				
	Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ				
	85721-0088, USA				
	Tel: 520 626 3967				
	Fax: 520 621 9288				
	Email: http://genome.arizona.edu				
	PCR Primers				
	FORWARD: gta aac cga cgg cca gtc				
	BACKWARD: gga aac agc tat gac cat g				
	Plate: 01 row: 3 column: 03				
	Seq primer: gta aac cga cgg cca gtc.				
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	/mol_type="mrna"				
	/cultivar="IR36"				
	/db_xref="taxon:39946"				
	/clone="OSIIEB01G03"				
	/issue="leaf"				
	/dev_stage="3 week"				
	/lab_host="DH10B"				
	/clone_lib="OSIIEB"				
	/note="Vector: plasmid II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (POG-6-3)"				
ORIGIN					

Query Match
 Best Local Similarity 28.5%; Score 261.6; DB 6; Length 585;
 Matches 363; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

Qy 76 ATGGGGAGGGGAGAGTAGATTAAGTAAAGTATGAGATTCGACGAAACAGGAGTAAAC 135
 Db 30 ATGGGGAGGGGAGAGTAGATTAAGTAAAGTATGAGATTCGACGAAACAGGAGTAAAC 135

Qy 136 TATTTCAAGAGAGAGTTGGGATCTAGAAAGGCGCAAGAGGCTCACTGTTCTTGTAT 195
 Db 90 TACTGAAAGCCCGGACGGGATCATGAAAGAGCGGAGGAGCTCCCGTCTTGTAT 195

Qy 196 GGTGAGTCTCTCTCATCATGTTCTCAAGACAGGAAAGTTGGCTGATTAATGACAGCC 255
 Db 150 GCCAGGTGGCCATCATGTTCTCTCCACCGGCAAGTACACAGAGTTGTCAGCCCT 209

Qy 256 TCTACTGATATTAAGGGGATATATGAGAGTACAGAGTTGTACTGAAATGATCTATGG 315
 Db 210 TCCACCGACATCAAGGGGATCTTGAACCGCTACCAAGCCATGCGCACAGCCCTTGG 269

Qy 316 AATGCTCAGATGAGAGATGCAATACGCTGAAGCATCTGATGATTAACCAAAAC 375
 Db 270 ATGAGAGATGATGAGATATGACAGCGACGCTGAGCCATCTCAAGACATCAACCGCAC 329

Qy 376 CTGAGGAGAGATTAAGAGAGAGGAGGAGAAAGTGAAGGAGGAGCATGATTAAGCAA 435
 Db 330 CTGCGGACCGAGATCAGCGCAAGAGTGGAGAGATCTGACGGGCTGAGTTCCAGCAG 389

Qy 436 CTGCGGAGTCTTGAGCAAACTTTGGAAGTCTCTTGAATGTTAGGCAATGAAGTAT 495
 Db 390 CTGCGGAGTCTTGAGCAAACTTTGGAAGTCTCTTGAATGTTAGGCAATGAAGTAT 495

Qy 496 CATGTGATGCGCACAACTGACACTTACAAGAAAGCTTAAAGCAAGAGGAAACT 555
 Db 450 CATGTGATGCGCACAACTGACACTTACAAGAAAGCTTAAAGCAAGAGGAAACT 555

Qy 556 TACCGCCCTCTAATATGATGATCTGATATGAAAGAGAGATCCGAGCATAG 607
 Db 510 TACAAAGCTCTGACAGCAGGAGCTGGGGTGTGTCGAGAGCGCGGCTGTTGG 561

RESULT 2
 CB971393 762 bp mRNA linear EST 30-Apr-2003
 LOCUS CAB10005_Ita_Fa_B07 Cabernet Sauvignon flower Pre-bloom - CAB1
 DEFINITION CB971393
 VERSION CB971393.1 GI:30254946
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 1 (bases 1 to 762)
 Jones, K. and Cook, D. Iandolo, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
 Goss, da Silva, F.,
 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon',
 berries at various developmental stages
 Unpublished (2003)
 Contact: Douglas Cook, PhD
 CARS Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcoc@ucdavis.edu
 Seq primer: ACGGTACCGACATATGCC.
 Location/Qualifiers
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 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultiyar="Cabernet Sauvignon"

ORIGIN
 Query Match
 Best Local Similarity 28.1%; Score 257.8; DB 6; Length 762;
 Matches 364; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

Qy 68 AGAGAGATGGGAGGAGAGATGAGTAAAGATTAAGATTCGACGAAACAGGC 127
 Db 2 AGGAGTGTATGGCTAGAGAGAGATTTGAGATCAAGAGATGAGAACTGAGGAAACAGGC 61

Qy 128 AAGTATCAATTTCTAAGAGAGAGTGGATTAAGTGAAGAGGCGCAAGAGCTCATCTTTC 187
 Db 62 AGGTACCTTCTCAAGAGAGAGATTTGATCTTCAAGAGGCGCAAGAGCTCATCTTTC 121

Qy 188 TCTGTATGCTCAGGTCTCTCATCATGTTCTTCAAGCAGAGAAAGTTGGCTGATTA 247
 Db 122 TTTGTATGCTCAGGTCTCTCATCATGTTCTTCAAGCAGAGAAAGTTGGCTGATTA 247

Qy 248 GCAAGCCCTCTAAGATTAAGGAGATTAAGAGGATTCAGAGGATTCGAGGATTAAG 307
 Db 182 TCAGCCCTTCACTACAGAGAGAGATTTGATCACTACAGAGATTCGAGGATTAAG 241

Qy 308 ATCTATGAGATGCTCTGATTAAGAGAGATTCAGAGATTCGAGGATTCGAGGATTA 367
 Db 242 ATCTATGAGATGCTCTGATTAAGAGAGATTCAGAGATTCGAGGATTCGAGGATTA 301

Qy 368 ACCAAAGCTGAGAGAGATTAAGAGAGAGAGAGAGAGATTCGAGGATTCGAGGATTA 427
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Qy 428 TAAAGCACTGGCGGCTTTGAGCAAACTTTGGAAGAGTCTCTTAAGATTTGATTAAG 487
 Db 362 TTGAGGAGTGGAGATTTGAGCAAACTTTGGAAGAGTCTCTTAAGATTTGATTAAG 421

Qy 488 GAAATATCATGTATGATGCGCACAACTGACACTTACAAGAAAGCTTAAAGCAACA 547
 Db 422 GGAAGTACAGGATGATCAATATCAAGATTTGAGCAAACTTAAAGCAACA 481

Qy 548 GGAAGTACAGGATGATCAATATCAAGATTTGAGCAAACTTAAAGCAACA 607
 Db 482 AAGCAATACCAAAATCTCTTCAAGATTTGAGCAAACTTAAAGCAACA 541

Qy 608 G 608
 Db 542 G 542

RESULT 3
 CB972246 692 bp mRNA linear EST 30-Apr-2003
 LOCUS CAB10006_Ita_Fa_D07 Cabernet Sauvignon flower Pre-bloom - CAB1
 DEFINITION CB972246
 VERSION CB972246.1 GI:30254946
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 BUKARYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 1 (bases 1 to 692)
 Jones, K. and Cook, D. Iandolo, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
 Goss, da Silva, F.,
 Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon',
 berries at various developmental stages
 Unpublished (2003)
 Contact: Douglas Cook, PhD
 CARS Genome Facility
 UC Davis, Plant Pathology
 One Shields Ave, Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcoc@ucdavis.edu
 Seq primer: ACGGTACCGACATATGCC.
 Location/Qualifiers
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 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /cultiyar="Cabernet Sauvignon"

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VERSION      CB972246.1  GI:30256403
KEYWORDS     EST.
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              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              rosids; Vitaceae; Vitis.
REFERENCE    1 (bases 1 to 692)
              Goes da Silva, F., Landolino, A., Lim, H., Baek, J., Leslie, A., Xu, J.,
              Jones, K. and Cook, D.
              Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
              berries at various developmental stages
              Unpublished (2003)
JOURNAL      Contact: Douglas Cook, PhD
              CAES Genome Facility
              UC Davis, Plant Pathology
              One Shields Ave, Davis, CA 95616, USA
              Tel: 530 754 6561
              Fax: 530 754 6617
              Email: drcoc@ucdavis.edu
              Seq primer: ACGGTACCGACATATGCC.
              Location/Qualifiers
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                /organism="Vitis vinifera"
                /mol_type="mRNA"
                /cultiar="Cabernet Sauvignon"
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                /dev_stage="Pre-bloom"
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                /note="Organ: Flower - Pre-bloom; Vector: pDON; Site: 1:
              Site 2: Site 1; CAB1 is a cDNA library of Vitis
              vinifera cv. 'Cabernet Sauvignon' clone 8 flowers. Samples
              were collected approximately eleven days before onset of
              bloom (clusters at this stage were fully developed and
              flowers with calypters or caps still attached. Sampled
              vines were located at the University of California, Davis,
              Experimental Vineyard. cDNAs were made by oligo-dT priming
              and directionally cloned. 5' and 3' adaptors were used in
              cloning as follows:
              5'-AAGCAGTGTATCAACGACGACGAGTGGCCATTACGGCGG-3' and
              5'-ATTCTAGAGCGCCGAGCGGCGGACATG-dt(30)NN-3'. Library was
              constructed using the Clontech Creator SMART kit and
              size-selected to contain the 0.5-3 kb size fraction."
ORIGIN
Query Match      27.8%; Score 255.2; DB 6; Length 692;
Best Local Similarity 65.4%; Pred. No. 2,7e-50;
Matches 374; Conservative 0; Mismatches 198; Indels 0; Gaps 0;

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12 AGAAGGATCTGAAATCGAGGAGAGAGAGAGAGTGTGCTAGAGAAAGATTGAG 71
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97 ATAAAAAAGATAGAGATCGACGAACAGGCAAGTTAATATTTCTAAGAGAGATTGG 156
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72 ATCAAGAGATAGAGAACTCGAAGAACAGGCAAGTCACTCACTCAAGAGAGAAATGCT 131
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157 ATATCTGAAGAGCCCAAGAGCTCATCTTCTCTGTGATGCTCAGAGTCTCTCATCATG 216
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
132 ATCTTCAAGAGGCGCAGTGAACCTCAGTCTTTGTGATGCTAAGGTTTCTATCATCATG 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
217 TTCTCAAGCAGAGAAAGTTGGCTGATTAATGAGCCCTCTAATGATTAAGGGGATA 276
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192 CTCTCCAGTACTGGAAGGCTCATGATATCATGAGCCCTTCCATCAAGAAACAAATA 251
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277 TATGAAGAGTACCAAGTGTGACTGAGATGATCTATGAGTCTCATGATGAGAGATG 336
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252 TTGTGATCAGTACAGAACTCTAGAGAGTGAATCTATGAGATCTATGAGAGATG 311
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337 CAGAAATACGCTGAAGCATCTGAATGATTAACCAAAACCTGAGAGAGAGATTAGAGG 396

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Qy          397 AGGAGGGGAGGAATTTGAGAGGCGATGACATTAAGCAACTGCGGCTTTGAGCAAACT 456
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db          372 AGGATGGGTGAACATTTGAGAGCGATTTGAGCGTTGAGAGAACTGGAGATCTTGAACAAAG 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy          457 TTGGAAGAGTCTTTGAAATTTGTTAGCATGAAAGTATATGATGTCGACACAAACT 516
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db          432 ATGAGAGTCTTTGAAAGATGTTGCTGATGAGAGATACCGAGTGAATCAATATCAGATT 491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy          517 GACACTTACAAAGAAAGCTTAAGACACAAAGGAACTTACCGCCCTTAATATACATGAA 576
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db          492 GAACTTTCAAGAAAACGGTAAAGATGTCGAAACAAATATACAAAAATCTCTCATGAA 551
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy          577 CTGATATGAAAGAGAGAAATCCGACTACGG 608
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db          552 TTGTATGCAAGGACAGAGATCAATTTATGG 583
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
CB921382
LOCUS       694 bp mRNA linear EST 25-APR-2003
DEFINITION VVD070D08 353397 An expressed sequence tag database for abiotic
              stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
              cDNA clone VVD070D08 5, mRNA sequence.
ACCESSION  CB921382.1 GI:30136044
VERSION    CB921382
KEYWORDS   EST.
SOURCE     Vitis vinifera
ORGANISM   Vitis vinifera
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; Vitaceae; Vitis.
            1 (bases 1 to 694)
REFERENCE  1
            Cushman, J.C.
            An expressed sequence tag database for abiotic stressed berries of
            Vitis vinifera var. Chardonnay
            Unpublished (2002)
JOURNAL    Contact: Cushman JC
            Department of Biochemistry
            University of Nevada
            MS200, Reno, NV 89557-0014, USA
            Tel: 775-784-1918
            Fax: 775-784-1650
            Email: jcushman@unr.edu
PCR PRIMER
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 070 row: D column: 08
Seq primer: T3 20mer
High quality sequence stop: 694.
Location/Qualifiers
  1..694
  /organism="Vitis vinifera"
  /mol_type="mRNA"
  /db_xref="taxon:29760"
  /clone="VVD070D08"
  /issue_type="Berries"
  /dev_stage="mixed: 8, 9, 11, 13, 15, 16 weeks dat"
  /clone_lib="An expressed sequence tag database for abiotic
  stressed berries of Vitis vinifera var. Chardonnay"
  /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
  EcoRI; Site_2: XhoI"
ORIGIN
Query Match      27.4%; Score 250.8; DB 6; Length 694;
Best Local Similarity 61.3%; Pred. No. 3.1e-49;
Matches 424; Conservative 0; Mismatches 262; Indels 6; Gaps 1;

79 GGGAGGGGAGATAGATTAATAAAGATGAGAAATCCGACGAACAGGCAAGTTACATAT 138
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db          1 GGTCTGGGAGAGTTGAGATCAAGAGATGAGAAACCCACCAACAGGACGTCACCTAC 60

```


SOURCE ORGANISM	Triticum aestivum (bread wheat) Triticum aestivum
REFERENCE AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 645) Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hefi, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J., Seaton, C.L. and Tong, J.C. The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library Unpublished (2000)
JOURNAL COMMENT	Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oanders@pw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: StrataGene SK primer.

```

FEATURES
SOURCE

Location/Qualifiers
1. 645
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE955_D02_G03"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOUR"
/clone_id="wheat pre-anthesis spike cDNA library"
/vector="Lambda Uni-ZAP XR, excised phagemid,
Site_1: EcoRI, Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give phuscript
phagemids in the T7 Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

```

ORIGIN

Query Match	26.0%	Score	238.6	DB 2	Length	645
Best Local Similarity	67.0%	Pred.	2.6e-46			
Matches	356	Conservative	0	Mismatches	169	Indels
						Gaps
						1
QY	73	GAGATGGGAGGGGGAAGATGAGATGAAAAAGATAGAAATCCGACGACGCAAGTT	132			
Db	105	GAGATGGGGGGGGGAAGATGAGATGAAAGGGAGTCGAAACGCCAAGACGCGAGGTG	164			
QY	133	ACATATTTCTAAGAGAGAGATTGGGATCTGAAAGAAAGCCAGAGAGCTCACTGTTCTGT	192			
Db	165	ACCTACTTCMAAGCCCGGTCCGGGATCATGAAAGGCGCGGAGACTCACCGTCTCTGC	224			
QY	193	GATGCTAGGCTCTGCTCATGATGTTTCMAAGCACAGAAAGTTGGCTGATTAATCCGACG	252			
Db	225	GACGCCAGGTGCGCATCATATGTTCTTCTTCACCGGCAAGTACACAGAGTTCTGCAGC	284			
QY	253	CCCTCTACTGATATTTAAGGGGATATATGAGAGGTACCAAGTGTGTGACTCGAATGAGTCTA	312			
Db	285	ACGGGACACGACATCAAGGGGATCTTTGACCGCTACCGACAGGCCATGGGGACAGCCTG	344			
QY	313	TGGAATGCTCAGTATGAGAGATGCAATACGCTGAACATCTGATGAGATTAAACCA	372			
Db	345	TGATTCGAGCGTATGAGAAATATGACGCGCACGCTGACCAATCTCAAGACATCATATCG	404			
QY	373	AACTGGAAGAGGATTAAGAGAGGAAAGGGGAGCAATTGGAGGGCATGAGCACTAAG	432			
Db	405	AACCTGGCACCGAGAT-----CAGATGGGTGAAGATCTTGAGACCGCTGGAGTTTGAG	458			

QY 433 TAACGGGCGGCTCTTAGCAAACTTTGGAAAGCTCTTAGAATTGTAGGATGTAAG 492

Db 459 GAGCTGGCGGACTTGGACAAAATGTGATCCGCTCTCAAGAGCTTCCGACAGGAAG 518

QY 493 TATCATGTGATCGGCACACAACATGACACTTACACAAGAAAAAGCTTAAAGACACAAGGAA 552

Db 519 TATCATGTGATCACCACGACAGACTGGAACTTACAGAAGAAAGGTGAAGCATCTCCAGGAG 578

QY 553 ACTTACCGCGCTCTTAATACATGAACTGGATATGAAAAGAGGAATCCGAAC 603

Db 579 GCATTCAGAAAGATCTGCAGCAGAGACTGGGTATGGCGCAGAGACCGGCGCTTAC 629

RESULT 7	CA732396	605 bp	mRNA	linear	EST 26-NOV-2002
LOCUS	CA732396				
DEFINITION	CA732396				
	wipic.pX005.m21 wipic Triticum aestivum cdna clone wipic.pX005.m21				
	5' end, mRNA sequence.				
ACCESSION	CA732396				
VERSION	CA732396.1	GI:25547994			
KEYWORDS	EST.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 605)
Tingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanfey, M. K.
Dupont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey

E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-651-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
M13(-) (-20.3155)

FEATURES	Location/Qualifiers
source	1. .605

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/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="w1p1c.pk005.m21"
/issue_type="lemma and palea"
/lab_host="DH10B"
/clone_lib="w1p1c"
/note="Vector: p Bluescript SK+ Site_1: EcoRI, Site_2:
XhoI; Wheat (Triticum aestivum, Hi Line) lemma and palea"

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ORIGIN

	Query Match	Similarity	25.9%	Score 237.8	DB 6	Length 605
	Match	Local Similarity	67.7%	Pred. No. 4e-46		
	Bases 329	Conservative	0	Mismatches 157	Indels 0	Gaps 0
QY	73	GAGATGGGGAGGGGGAAGATGAGATATAAAAAGATTAGAAATCCGACGAACAGGCAACTT				132
Db	111	GAGATGGGGCGGGGGGAAGATTGAAATTAAGCGGATCGAAGACGGACCAACAGGACAGGTG				170
QY	133	ACATATTTCTAAGAGAGAGATTGGGATCTGTAAGAAAGGCGAAGAGCTCAGTCTCTCGT				192
Db	171	ACCTACTTCAGACCGCCCGGTCCGGGGATCATGAGAGAGGGCGGGAGACTCACGTGCTTCGC				230
QY	193	GAGTCTCAGGTCTCTCTCATCATGTTCTCAAGCACAGAGAAAGTTGGCTGATTAATGTCAGC				252
Db	231	GACGCCACAGGTCGCATCATCATATTTCTCCGCCACCGGCAAGTACCAAGATTTCTGCAGC				290
QY	253	CCCTCTCTGATATTATTAAGGGGATATTATGAGAGTAAACAGAGTTGGACTGGAATGGATCTA				312
Db	291	ACCGGCACCGCATCAAGGGGATTTTGAACCGCTACACGACGGCCATCGGGACCAAGCCTTG				350
QY	313	TGGAAATCTCAGTATGAGAGATGCAGAAATACGCTGAAGACATCTGAATGGAATTAACCA				372


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QY 675 GATGTTTCTTAGGGTTGTCATCCGAATCAGCCCAATCTGTTAGGTATAGA 734
DB 746 GGACATGTAGCCCTTCCTCCGCGTGGTCCAGCCAGCCCACTGACAGCATGCGCTTACG 805
QY 735 ATCAATGATGTTTACCTTCATTA 758
DB 806 CTTCACAGACCTCCGCTGGGCTTA 829

RESULT 11
CAS971172 605 bp mRNA linear EST 21-NOV-2002
LOCUS wpalc.pk016.11 wpalc Triticum aestivum cDNA clone wpalc.pk016.11 5'
DEFINITION end, mRNA sequence.
ACCESSION CAS971172
VERSION CAS971172.1 GI:25149628
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 605)
Tingey, S.V., Moore, G., Griffiths, S., Powell, W., Wolters, P.,
Dolan, M., Hainey, C., Mao, G., Caraher, N. and Hanafey, M.K.
Center 1
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
E. I. Dupont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Fax: 302-631-2602
Email: Scott.V.Tingey@usa.dupont.com
Seg primer: M13

FEATURES
Source location/Qualifiers
1..605
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wpalc.pk016.11"
/tissue_type="anthers"
/lab_host="MDH10B"
/clone_lib="wpalc"
/notes="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum) pre-meiotic anthers JIC"

ORIGIN
Query Match 25.4%; Score 232.6; DB 6; Length 605;
Best Local Similarity 66.0%; Pred. No. 76-45;
Matches 344; Conservative 0; Mismatches 171; Indels 6; Gaps 1;

QY 73 GAGATGGGGAGGGGAGATGAGATTAAGATAGAAATCCGACGAGCGCAAGTT 132
DB 83 GAGATGGGGAGGGGAGATGAGATTAAGATAGAAATCCGACGAGCGCAAGTT 132
QY 133 ACATATTCTTAAGAGAGAGTTGGGATATGAGAAAGCCCAAGAGCTCACTGTTCTGT 142
DB 143 ACCTACTCCAAGCGCGGTGGGATCATGAAGAGCGCGGAGAGCTCACTGTTCTGT 192
QY 193 GATGCTCAGGCTCTCTCATCATGTTCTCAAGACAGAGAAAGTTGGGCTGATTAATGACG 252
DB 203 GAGCGCCAGGTGCGCATCATGTTCTCTCCACCGGCAAGTACACAGAGTTCTGAGC 262
QY 263 CCTCTACTGATATTAAAGGGATATATAGAGATCCAGGTTGACTGGAATGATCTA 312
DB 263 ACCGGACCGACATCAAGGGATCTTTAACCCTACCAAGCGCATTCGAGACAGCTG 322
QY 313 TGAATGCTCAGTATAGAGATGAGATTAAGCTGAGAGCATCTGAATGATTAACCA 372
DB 323 TGGATGAGCGATGATGAGATTAAGAGCGACGCTGAGCATCTCAAGAGCATCAATCG 382

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QY 373 AACCTGAGAGAGATTAAGAGAGAGAGAGAGAGAGAAATTTGAGGGCATGACATAAG 432
DB 383 AACCTGAGAGAGATTAAGAGAGAGAGAGAGAGAGAGAAATTTGAGGGCATGACATAAG 436
QY 433 CAATCGCGGCTCTTGAAGCAAACTTGGAGAAAGTCTCTTGAATTTGAGCATAGAAAG 492
DB 437 GAGCTGCGGACCTTGAAGCAAACTTGAAGTCCGCTCTCAAGAGAGTTCCGACAGNNNAAG 496
QY 493 TATCATGATGATCGACCAAACTGACATTAAGAAAGAAAGCTTAAAGCAAGAGAA 552
DB 497 TATCATGATGATCGACCAAGAGAGAGAGAGAGAGAGAGAAAGAAAGAAAGAGAGAGAG 556
QY 553 ACTTACCGGCTCTTGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
DB 557 NCATACAGAGATCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597

RESULT 12
AJ803128 604 bp mRNA linear EST 11-AUG-2004
LOCUS AJ803128 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
DEFINITION 018_5_06_a10, mRNA sequence.
ACCESSION AJ803128
VERSION AJ803128.1 GI:51118456
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Aspetidae; Lamiales; Plantaginaceae; Antirrhinae;
Antirrhinum.
1 (bases 1 to 604)
Zachgo, S., Stueber, K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrhinum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzen-genetik
MPI fuer Zuechtungs-forschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
1..604
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_5_06_a10"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN
Query Match 24.9%; Score 228; DB 1; Length 604;
Best Local Similarity 61.7%; Pred. No. 8.8e-44;
Matches 363; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 23 GAGAGAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 82
DB 17 GAGAGAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 76
QY 83 GGGGAGATGAGATTAAGAAAGATTAAGAAATTCATTAAGAAATTAAGATGAGCTC 142
DB 77 GTGGAGATTCAGATTAAGAGATTAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 136
QY 143 AGAGAGAGGTTGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 202
DB 137 AGAGAGAGAGGTTGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
QY 203 TCTCTCATCATGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 262
DB 197 TTTCGTTATCATGATCTCAAGATCTCAAGAGATCTCAAGATCTCAAGATCTCAAG 256
QY 263 ATATTAAGGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 322
DB 257 CGACAAAGAGGTTTGTAGATTAAGATCAACATGCTGTTGAGAGTTGATCTTGAACAC 316

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QY 323 AGTATGAGAGATGCAATACGCTGAGCATCTGTAATGATTAACCAAACTTGAGA 382
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 DB 317 ACTACAGAAAAGACAGAGCATTTGAAAGCTTAAAGAGATTAACAGGAATCTCGGA 376
 |||||
 QY 383 AGGAGATTAGAGAGAGAGAGAGAGATTGGAGGGCATGACATTAAGCAACTGGCG 442
 |||||
 DB 377 AGGAGATTAGAGAGAGAGAGAGAGATTGGAGGGCATGACATTAAGCAACTGGCG 436
 |||||
 QY 443 GTCTTACGCAAACTTTGGAAAGTCTTTAGAAATGTTAGGCATAGAAAGTATCATGTGA 502
 |||||
 DB 437 ATCTCATGGAAGAAATGATTAATCTCTCAGGGTCATCTGGAAGAAATATTAAGTCA 496
 |||||
 QY 503 TGGCCACACAACTGACATTTACAGAAAAAGCTTAAAGCACAAGGAAACTTACCGCG 562
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 DB 497 TTGGTATATCAAAATCGAAACCAAGCAAGAAAGGTGAGAAAAGTGAAGAAATATACAGGA 556
 |||||
 QY 563 CTCTAATACATGAATCGATATGATAAGAGAGATCCGACTACGGTT 610
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 DB 557 GCCTAATGCTCGAATATGATACATACAGAGAGATCCACACTTTGGAT 604
 |||||

RESULT 13
 CB087977 642 bp mRNA linear EST 27-JAN-2003
 LOCUS hk10f10.g1 Hedycotis centranthoides flower - Stage 2 (NTBG) Hedycotis
 DEFINITION centranthoides cDNA clone hk10f10, mRNA sequence.
 CB087977 GI:27912169

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Hedycotis centranthoides
 Hedycotis centranthoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Gentianales; Rubiaceae; Rubioidae;
 Spermacoceae; Hedycotis.

REFERENCE
 AUTHORS
 1 (bases 1 to 642)
 Levesque,M.P., Twiss,R.W., Mottley,T., Katarci,M.S., Dedhia,N.N.,
 O'Shaughnessy,A.L., Ballia,V., Martienssen,R.A., McCombie,R.W.,
 Benfey,P. and Stevenson,D.
 Expressed tag sequences from Hedycotis centranthoides flower - Stage
 2 (NTBG)

TITLE
 2 (NTBG)

JOURNAL
 COMMENT
 Unpublished (2003)
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8874
 Fax: 516 367 8874
 Email: mcombie@cshl.org

FEATURES
 source
 1.642
 Location/Qualifiers
 /organism="Hedycotis centranthoides"
 /mol_type="mRNA"
 /db_xref="taxon:219666"
 /clone="hk10f10"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_1b="Hedycotis centranthoides flower - Stage 2
 (NTBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site_1: XhoI;
 Site_2: Eco RI; Date: Completed 12/18/01. Submitted to
 SCSL 12/21/01 Library: Stratsgene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG Herbarium voucher TW2563"

ORIGIN
 Query Match 24.8%; Score 227.4; DB 6; Length 642;
 Best Local Similarity 62.3%; Pred. No. 1,2e-43;
 Matches 357; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

QY 36 GAGACAGAGAGAAAAACAGGGGAGAACAGGGGAAAGAGATGGGGAGGGGAAAGTACA 95
 |||||
 DB 68 GAGATCAAAAGACGAAAGAGAAAGAAAGAAACCAAAAAAGAAATGGCTCGTGGAAAGTCCA 127
 |||||
 QY 96 GATAAAAAAGATAGAAATCCGACGAACAGGCAAGTAACTATTTTAAGAGAGATTGG 155
 |||||
 DB 128 GATCAAGAGATTGAAATCAGACTTAACAGGCAAGTGAATTACTTCAAGAAAGAAATGG 187
 |||||
 QY 156 GATACAGAAAGAGCCAGAGAGCTCACTGTTCTGTGTGATGCTCAGGTCTCTCATCAT 215
 |||||
 DB 188 GCTTTTAAAGAAAGTCATGAGCTCACCGTTTGTGTGATGATTAAGGTCTCCATCTCAT 247
 |||||
 QY 216 GTTCTCAAGCAGAGAAAGTTGGCTGATTAATCTGACAGCCCTCTACTGATATTAAGGGAT 275
 |||||
 DB 248 GATTTCACATCCACCAAGCTTCATAGTACATCAATCAGTCTTTATCTCGACGAAGAGAT 307
 |||||
 QY 276 ATATGAGAGGTACAGATTGTGACTGTAATGATATGATGAAATGCTCAGTATGAGAGAT 335
 |||||
 DB 308 GGTGATCTGTATCAAGAAATGCTTTAGGGGTGATATATGAACTCATATGAGAGAT 367
 |||||
 QY 336 GCAGAAATACGCTGAGACATCTGAATGATTAACCAAACTGAGAGAGAGATTAAGAG 395
 |||||
 DB 368 GCAAGAAACATTAAGAAAGTTGAAGAGATGAAATGAAGATCTTGTATGAGATGAGACA 427
 |||||
 QY 396 GAGGAAAGGGGAGAGAAATTTGAGGCGATGACATTAAGCAACTGCGCGCTTTAGCAAAAC 455
 |||||
 DB 428 GAGGATGGGGGAGAGCTTAATGATCTGATATGATATGATGATGCTGCTTCATTGAAGA 487
 |||||
 QY 456 TTGGAAGAGTCTCTAGAAATGTTAGGCAATGAAGATATCATGTATGCGCACACAAAC 515
 |||||
 DB 488 TGTGACAAATTCAGTTGAGATCAATTCGGAGAGAGAAAGCTTAAGATATTCGCAATCAAT 547
 |||||
 QY 516 TGACACTTACAGAAAGAAAGCTTAAAGACCAAGGAAAGCTTAACCGGCTTATATACATGA 575
 |||||
 DB 548 CGACACTTACAGAAAGAAAGTTAGAAATGTTAGAGAGATACACAGAAATCTCTGCAGGA 607
 |||||
 QY 576 ACTGATATGAAGAGAGAGATTCGAATCAACG 608
 |||||
 DB 608 ATTGATGCCCGACAGAAAGATCCACATATGG 640
 |||||

RESULT 14
 BUB77396 605 bp mRNA linear EST 16-OCT-2002
 LOCUS V033E07 Populus flower cDNA library Populus balsamifera subsp.
 DEFINITION trichocarpa cDNA 5 prime, mRNA sequence.
 BUB77396

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 BUB77396.1 GI:24068920
 EST.
 Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
 Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

REFERENCE
 AUTHORS
 1 (bases 1 to 605)
 Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished (2002)

JOURNAL
 COMMENT
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
 source
 1.605
 Location/Qualifiers
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"

ORIGIN
 Query Match 24.8%; Score 227.4; DB 6; Length 642;
 Best Local Similarity 62.3%; Pred. No. 1,2e-43;
 Matches 357; Conservative 0; Mismatches 216; Indels 0; Gaps 0;

